



SEQUENCE LISTING

<110> HOOK, Magnus

<120> BIOINFORMATIC METHOD FOR IDENTIFYING SURFACE-ANCHORED PROTEINS FROM GRAM-POSITIVE BACTERIA

<130> P07741US01/BAS

<140> 10/661809

<141> 2003-09-15

<150> 60/410303

<151> 2002-09-13

<160> 24

<170> PatentIn version 3.1

<210> 1

<211> 5

<212> PRT

<213> *Staphylococcus epidermidis*

<220>

<221> MISC\_FEATURE

<222> (3)..(3)

<223> X = any amino acid

<400> 1

Leu Pro Xaa Thr Gly  
1 5

<210> 2

<211> 777

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 2

Gln Glu Gln Thr Ala Lys Glu Asp Val Ala Asp Ser Ala Thr Ser Val  
1 5 10 15

Gly Ala Ile Val Ser Ile Glu Lys Ala Glu Lys Asn Phe Val Ile Thr  
20 25 30

Tyr Ala Ser Gly Lys Lys Ala Gln Ile Ser Ile Leu Asn Asp His Leu  
35 40 45

Phe Arg Tyr His Leu Asp Pro Thr Gly Lys Phe Glu Glu Tyr Pro Thr  
50 55 60

Pro Asn Asp Pro Lys His Val Ala Lys Ile Thr Ala Lys Thr Met Ala  
65 70 75 80

Asp Tyr Gly Thr Gln Ala Phe Glu Gln Thr Asn Val Thr Asp Ser Gly  
85 90 95

Asn Gln Phe Ile Leu Glu Asn Asn Gly Leu Lys Ile Met Phe Glu Lys  
100 105 110

Glu Ser Ala Leu Met Lys Val Leu Asp Lys Lys Lys Asn Gln Val Ile  
115 120 125

Leu Glu Glu Thr Ala Pro Leu Ser Phe Lys Asn Asp Lys Ala Thr Gln  
130 135 140

Thr Leu Lys Gln Ser Ser Gln Glu Asn Tyr Phe Gly Gly Gly Thr Gln  
145 150 155 160

Asn Gly Arg Phe Thr His Lys Gly Thr Ala Ile Gln Ile Val Asn Thr  
165 170 175

Asn Asn Trp Val Asp Gly Gly Val Ala Ser Pro Asn Pro Phe Tyr Trp  
180 185 190

Ser Thr Ala Gly Tyr Gly Val Val Arg Asn Thr Trp Lys Pro Gly Asn  
195 200 205

Tyr Asp Phe Gly Ser His Asp Pro Gln Lys Thr Thr Thr His Glu  
210 215 220

Gly Thr Asp Phe Asp Ala Phe Tyr Phe Phe Asn Asp Ser Ser Ala Gly  
225 230 235 240

Ile Leu Lys Asp Tyr Tyr Glu Leu Thr Gly Lys Pro Ala Leu Met Pro  
245 250 255

Glu Tyr Gly Phe Tyr Glu Ala His Leu Asn Ala Tyr Asn Arg Asp Tyr  
260 265 270

Trp Val Lys Val Ala Glu Gly Thr Ala Gly Ala Val Lys Phe Glu Asp  
275 280 285

Gly Asn Phe Tyr Lys Glu Tyr Gln Pro Gly Asp Leu Gly Asn Leu Asn  
290 295 300

Gly Thr Leu Glu Ser Leu Asn Gly Glu Lys Glu Asn Tyr Gln Phe Ser  
305 310 315 320

Ala Arg Ala Val Ile Asp Arg Tyr Lys Lys Asn Asp Met Pro Leu Gly  
325 330 335

Trp Phe Leu Pro Asn Asp Gly Tyr Gly Ala Gly Tyr Gly Gln Thr Asp  
340 345 350

Ser Leu Asp Gly Asp Val Gln Asn Leu Lys Glu Phe Thr Glu Tyr Ala  
355 360 365

Gln Ala Asn Gly Val Glu Val Gly Leu Trp Thr Gln Ser Asn Leu His  
370 375 380

Pro Ala Asp Pro Lys Asn Pro Lys Lys Gly Glu Arg Asp Ile Ala Lys  
385 390 395 400

Glu Val Ser Val Ala Gly Val Lys Ala Leu Lys Thr Asp Val Ala Trp  
405 410 415

Val Gly Tyr Gly Tyr Ser Phe Gly Leu Asn Gly Val Glu Asp Ala Ala  
420 425 430

Asn Val Phe Val Lys Glu Thr Asp Gly Ala Val Arg Pro Met Ile Val  
435 440 445

Ser Leu Asp Gly Trp Ala Gly Thr Gln Arg His Ala Gly Ile Trp Thr  
450 455 460

Gly Asp Gln Thr Gly Gly Gln Trp Glu Tyr Ile Arg Phe His Ile Pro  
465 470 475 480

Thr Tyr Ile Gly Thr Ser Leu Ser Gly Gln Pro Asn Val Gly Ser Asp  
485 490 495

Met Asp Gly Ile Phe Gly Gly Lys Asn Lys Glu Ile Asn Ile Arg Asp  
500 505 510

Phe Gln Trp Lys Thr Phe Thr Pro Val Gln Leu Asn Met Asp Gly Trp  
515 520 525

Gly Ser Asn Pro Lys Thr Pro Phe Ala Phe Asp Gln Glu Ala Thr Asp  
530 535 540

Leu Asn Arg Ala Tyr Leu Lys Leu Lys Ser Met Met Met Pro Tyr Asn  
545 550 555 560

Tyr Ser Ile Ala Lys Glu Ser Val Asp Gly Leu Pro Met Val Arg Ala  
565 570 575

Met Ala Leu Glu Phe Pro Asn Glu Gly Thr Ala Tyr Thr Lys Asp Ser  
580 585 590

Gln Tyr Gln Tyr Met Trp Gly Pro Asn Leu Leu Val Ala Pro Ile Tyr  
595 600 605

Asn Gly Asn Gln Asp Glu Ala Gly Asn Ser Ile Arg Asp Gly Ile Tyr  
610 615 620

Leu Pro Asp Glu Lys Gln Val Trp Val Asp Leu Phe Thr Gly Glu Lys  
625 630 635 640

Tyr Gln Gly Gly Arg Val Leu Asn Gly Val Lys Thr Pro Leu Trp Lys  
645 650 655

Val Pro Val Phe Val Lys Asp Gly Ser Ile Ile Pro Met Thr Asn Pro  
660 665 670

Asn Asn Asn Pro Lys Glu Ile Gln Arg Asp Gln Arg Ser Phe Leu Ile  
675 680 685

Tyr Pro Asn Gly Thr Thr Ser Phe Asn Met Tyr Glu Asp Asp Gly Ile  
690 695 700

Ser Thr Ser Tyr Glu Ala Gly Gln Ser Ala Thr Thr Lys Ile Asn Ser  
705 710 715 720

Gln Gly Pro Lys Ser Asn Glu Lys Gly Asp Leu Thr Val Thr Ile Glu  
725 730 735

Pro Thr Lys Gly Ser Tyr Lys Asp Phe Val Asp Glu Arg Ser Thr Thr

740

745

750

Leu Asp Leu Leu Ala Ser Glu Ala Pro Glu Ser Val Thr Ala Met Val  
755 760 765

Gly Gly Thr Glu Val Thr Leu Lys Gln  
770 775

<210> 3  
<211> 1010  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 3

Ala Ala Asn Lys Glu Glu Phe Leu Ala Gly Thr Asn Leu Tyr Tyr Phe  
1 5 10 15

Asp Lys Glu Phe Gln Val Asn Gln Tyr Leu Ser Glu Ala Ser Gly Glu  
20 25 30

Lys Leu Asn Gln Ser Ala Leu Ser Val Lys Leu Ala Lys Gln Ser Val  
35 40 45

Thr Ala Lys Asp Val Gln Ile Thr Val Lys Gly Phe Ile Asn Lys Gly  
50 55 60

Thr Val Asp Gly Gly Asn Thr Thr Val Asp Asp Gln Leu Thr Ile Pro  
65 70 75 80

Ala Asn Val Ala Ile Asn Glu Glu Lys Thr Thr Pro Ser Ser Leu Thr  
85 90 95

Leu Gln Trp Asp Gln Val Thr Glu Ala Thr Ser Tyr Glu Val Glu Arg  
100 105 110

Asp Gly Thr Val Phe Gly Asn Ile Gln Thr Asn Thr Ala Thr Phe Asp  
115 120 125

Gly Phe Ser Phe Leu Ser Glu His Thr Phe Arg Val Arg Ala Val Gly  
130 135 140

Lys Asn Gly Val Ser Glu Trp Ser Glu Pro Ile Lys Gly Lys Thr Gln  
145 150 155 160

Asp Asp Pro Tyr Lys Glu Thr Ile Asn Gln Val Lys Ala Thr Ser Asn  
165 170 175

Leu Pro Glu Gln Pro Gly Ala Glu Leu Lys Lys Leu Thr Asp Lys Asp  
180 185 190

Leu Ser Thr Gly Trp His Thr Asn Trp Ser Thr Gly Ile Ala Asn Pro  
195 200 205

Ser Asp Gly Asn Phe Leu Ser Leu Lys Phe Asp Leu Gly Ala Glu Tyr  
210 215 220

Gln Met Asp Lys Ile Glu Tyr Leu Pro Arg Asp Asn Ala Gly Asn Gly  
225 230 235 240

Asn Ile Leu Gln Leu Gln Tyr Arg Thr Ser Lys Asp Gly Ala Asn Trp  
245 250 255

Thr Glu Phe Ser Glu Pro Ile Asn Trp Lys Gln Asp Ala Leu Thr Lys  
260 265 270

Thr Ile Glu Thr Lys Asp Gln Ala Tyr Arg Phe Val Glu Met Lys Val  
275 280 285

Leu Lys Ser Val Gly Asn Phe Gly Ser Gly Arg Glu Met Leu Phe Tyr  
290 295 300

Lys Gln Pro Gly Thr Glu Gly Ile Leu His Gly Asp Ile Thr Asn Asp  
305 310 315 320

Gly Thr Ile Asp Glu Asn Asp Ala Met Ser Tyr Arg Asn Tyr Thr Gly  
325 330 335

Leu Glu Ser Val Asp Ser Asp Phe Asn Gly Tyr Val Glu Lys Gly Asp  
340 345 350

Leu Asn Lys Asn Gly Val Ile Asp Ala Tyr Asp Ile Ser Tyr Val Leu  
355 360 365

Arg Gln Leu Asp Gly Gly Ile Glu Ile Pro Asp Val Glu Glu Ile Ala  
370 375 380

Gly Gly Leu Ser Leu Ala Val Val Asn Glu Asn Gly Lys Asp Thr Tyr  
385 390 395 400

Leu Pro Gly Asp Thr Leu Thr Phe Ile Leu Lys Gly Gln Asp Leu Lys  
405 410 415

Asn Ile Asn Ala Leu Ser Thr Lys Met Ser Phe Asp Ser Ser Lys Phe  
420 425 430

Glu Leu Val Gly Gln Pro Ala Thr Thr Asn Asn Thr Gln Gln Met Glu  
435 440 445

Asn Tyr Ser Lys Tyr Arg Lys His Ser Asn Asp Val Glu Asn Leu Tyr  
450 455 460

Leu Val Leu Ser Asn Gln Gly Asn Lys Gln Leu Leu Asn Gly Ser Met  
465 470 475 480

Asp Leu Val Thr Phe Lys Val Lys Glu Thr Thr Arg Val Lys  
485 490 495

Arg Ala Thr Thr Val Glu Gln Pro Leu Gln Phe Asp Met Ser Gln Gly  
500 505 510

Leu Leu Val Gly Gln Gly Phe Gln Gln Ala Thr Leu Ser Asp Phe Ser  
515 520 525

Val Thr Val Lys Pro Thr Glu Leu Val Asp Lys Glu Leu Leu Gln Ala  
530 535 540

Leu Ile Thr Leu Asn Gln Ala Arg Val Glu Lys Glu Tyr Thr Pro Glu  
545 550 555 560

Thr Trp Ala Ile Phe Lys Pro Ile Leu Asp Glu Ala Val Ala Val Leu  
565 570 575

Ala Asn Glu Gln Ala Thr Gln Thr Asp Val Ser Ala Ala Ala Glu Asn  
580 585 590

Leu Glu Lys Ala Ala Ser Gln Leu Glu Lys Met Pro Asp Val Ala Asn  
595 600 605

Lys Ala Asp Leu Glu Lys Ala Ile Gln Glu Gly Leu Ala Lys Lys Pro

610 615 620

Ser Asp Gly Gln Glu Phe Thr Glu Glu Thr Lys Lys Val Leu Glu Glu  
625 630 635 640

Ser Leu Ala Ala Ala Gln Lys Val Phe Ala Gln Glu Lys Val Thr Gln  
645 650 655

Glu Glu Ile Asp Gln Ala Thr Lys Thr Leu Arg Glu Ala Ile Ala Gln  
660 665 670

Leu Lys Glu Gln Pro Val Ala Val Asp Lys Glu Thr Leu Lys Glu Gln  
675 680 685

Ile Ala Gln Ala Arg Gly Arg Lys Pro Glu Glu Gly Tyr Gln Phe Thr  
690 695 700

Lys Glu Thr Glu Lys Gln Leu Gln Glu Ala Ile Gln Ala Ala Glu Ala  
705 710 715 720

Ile Val Ala Lys Glu Thr Ala Thr Lys Glu Glu Val Ser Glu Ala Leu  
725 730 735

Asn Ala Leu Glu Thr Ala Met Ala Gln Leu Lys Glu Val Pro Leu Val  
740 745 750

Asn Lys Asp Gln Leu Gln Glu Val Val Lys Arg Ala Gln Gln Val Thr  
755 760 765

Pro Ser Glu Gly His Gln Phe Thr Ala Ser Ser Leu Gln Glu Leu Gln  
770 775 780

Lys Ala Leu Leu Ala Ala Lys Asn Thr Leu Lys Asn Pro Ala Ala Asn  
785 790 795 800

Gln Lys Met Ile Asp Glu Ala Val Ala Glu Leu Thr Ser Ala Ile Asp  
805 810 815

Gly Leu Gln Glu Glu Val Leu Val Thr Asp Lys Lys Ala Leu Glu Ala  
820 825 830

Met Ile Ala Lys Ala Lys Ala Ile Lys Pro Ser Ala Gly Lys Glu Phe  
835 840 845

Thr Ser Glu Ser Lys Ala Arg Leu Thr Glu Ala Ile Asp Gln Ala Glu  
850 855 860

Gly Ile Leu Ala Asp Lys Asn Ala Arg Gln Glu Gln Ile Asp Ile Ala  
865 870 875 880

Glu Lys Asn Val Lys Thr Ala Leu Asp Ser Leu Glu Glu Gln Val Leu  
885 890 895

Gln Thr Asp Lys Thr Lys Leu Lys Glu Leu Leu Gln Lys Ala Glu Thr  
900 905 910

Leu Lys Pro Lys Ala Gly Lys Gln Phe Thr Lys Ala Ser Gln Glu Ala  
915 920 925

Leu Ala Glu Ala Ile Lys Gln Ala Lys Ala Leu Val Glu Asp Pro Asn  
930 935 940

Ala Thr Gln Glu Ala Val Asp Lys Cys Leu Ser Ile Leu Ser Gln Ala  
945 950 955 960

Ile Glu Ala Met Ala Glu Glu Pro Ile Ser Ser Asn Ser Thr Gly Asn  
965 970 975

Asn Gly Asn His Ser Thr Val Ser Gly Thr Gly Gly Val Thr Ser Gln  
980 985 990

Gly Lys Gly Thr Ala Thr Gly Gly Thr Thr Thr Lys Thr Thr Thr Ser  
995 1000 1005

Gly Thr  
1010

<210> 4  
<211> 1108  
<212> PRT  
<213> Staphylococcus epidermidis

<400> 4

Glu Glu Val Asn Ser Asp Gly Gln Leu Thr Leu Gly Glu Val Lys Gln  
1 5 10 15

Thr Ser Gln Gln Glu Met Thr Leu Ala Leu Gln Gly Lys Ala Gln Pro  
20 25 30

Val Thr Gln Glu Val Val Val His Tyr Ser Ala Asn Val Ser Ile Lys  
35 40 45

Ala Ala His Trp Ala Ala Pro Asn Asn Thr Arg Lys Ile Gln Val Asp  
50 55 60

Asp Gln Lys Lys Gln Ile Gln Ile Glu Leu Asn Gln Gln Ala Leu Ala  
65 70 75 80

Asp Thr Leu Val Leu Thr Leu Asn Pro Thr Ala Thr Glu Asp Val Thr  
85 90 95

Phe Ser Tyr Gly Gln Gln Arg Ala Leu Thr Leu Lys Thr Gly Thr  
100 105 110

Asp Pro Thr Glu Ser Thr Ala Ile Thr Ser Ser Pro Ala Ala Ser Ala  
115 120 125

Asn Glu Gly Ser Thr Glu Glu Ala Ser Thr Asn Ser Ser Val Pro Arg  
130 135 140

Ser Ser Glu Glu Thr Val Ala Ser Thr Thr Lys Ala Ile Glu Ser Lys  
145 150 155 160

Thr Thr Glu Ser Thr Thr Val Lys Pro Arg Val Ala Gly Pro Thr Asp  
165 170 175

Ile Ser Asp Tyr Phe Thr Gly Asp Glu Thr Thr Ile Ile Asp Asn Phe  
180 185 190

Glu Asp Pro Ile Tyr Leu Asn Pro Asp Gly Thr Pro Ala Thr Pro Pro  
195 200 205

Tyr Lys Glu Asp Val Thr Ile His Trp Asn Phe Asn Trp Ser Ile Pro  
210 215 220

Glu Asp Val Arg Glu Gln Met Lys Ala Gly Asp Tyr Phe Glu Phe Gln  
225 230 235 240

Leu Pro Gly Asn Leu Lys Pro Asn Lys Pro Gly Ser Gly Asp Leu Val

245	250	255
Asp Ala Glu Gly Asn Val Tyr Gly Thr Tyr Thr Ile Ser Glu Asp Gly		
260	265	270
Thr Val Arg Phe Thr Phe Asn Glu Arg Ile Thr Ser Glu Ser Asp Ile		
275	280	285
His Gly Asp Phe Ser Leu Asp Thr His Leu Asn Asp Ser Asp Gly Arg		
290	295	300
Gly Pro Gly Asp Trp Val Ile Asp Ile Pro Thr Gln Glu Asp Leu Pro		
305	310	315
320		
Pro Val Val Ile Pro Ile Val Pro Asp Thr Glu Gln Gln Ile Asp Lys		
325	330	335
Gln Gly His Phe Asp Arg Thr Pro Asn Pro Ser Ala Ile Thr Trp Thr		
340	345	350
Val Asp Ile Asn Gln Ala Met Lys Asp Gln Thr Asn Pro Thr Val Thr		
355	360	365
Glu Thr Trp Pro Thr Gly Asn Thr Phe Lys Ser Val Lys Val Tyr Glu		
370	375	380
Leu Val Met Asn Leu Asp Gly Thr Ile Lys Glu Val Gly Arg Glu Leu		
385	390	395
400		
Ser Pro Asp Glu Tyr Thr Val Asp Lys Asn Gly Asn Val Thr Ile Lys		
405	410	415
Gly Asp Thr Asn Lys Ala Tyr Arg Leu Glu Tyr Gln Thr Thr Ile Asp		
420	425	430
Glu Ala Val Ile Pro Asp Gly Gly Asp Val Pro Phe Lys Asn His		
435	440	445
Ala Thr Leu Thr Ser Asp Asn Asn Pro Asn Gly Leu Asp Ala Glu Ala		
450	455	460
Thr Val Thr Ala Thr Tyr Gly Lys Met Leu Asp Lys Arg Asn Ile Asp		
465	470	475
480		

Tyr Asp Glu Ala Asn Gln Glu Phe Thr Trp Glu Ile Asn Tyr Asn Tyr  
485 490 495

Gly Glu Gln Thr Ile Pro Lys Asp Gln Ala Val Ile Thr Asp Thr Met  
500 505 510

Gly Asp Asn Leu Thr Phe Glu Pro Asp Ser Leu His Leu Tyr Ser Val  
515 520 525

Thr Phe Asp Asp Lys Gly Asn Glu Val Val Gly Ala Glu Leu Val Glu  
530 535 540

Gly Lys Asp Tyr Lys Val Val Ile Asn Gly Asp Gly Ser Phe Ala Ile  
545 550 555 560

Asp Phe Leu His Asp Val Thr Gly Ala Val Lys Ile Asp Tyr Lys Thr  
565 570 575

Lys Val Asp Gly Ile Val Glu Gly Asp Val Ala Val Asn Asn Arg Val  
580 585 590

Asp Val Gly Thr Gly Gln His Ser Glu Asp Asp Gly Thr Ala Ser Gln  
595 600 605

Gln Asn Ile Ile Lys Asn Thr Gly Ala Val Asp Tyr Gln Asn Ser Thr  
610 615 620

Ile Gly Trp Thr Leu Ala Val Asn Gln Asn Asn Tyr Leu Met Glu Asn  
625 630 635 640

Ala Val Ile Thr Asp Thr Tyr Glu Pro Val Pro Gly Leu Thr Met Val  
645 650 655

Pro Asn Ser Leu Val Val Lys Asp Thr Thr Thr Gly Ala Gln Leu Thr  
660 665 670

Leu Gly Lys Asp Phe Met Val Glu Ile Thr Arg Asn Ala Asp Gly Glu  
675 680 685

Thr Gly Phe Lys Val Ser Phe Ile Gly Ala Tyr Ala Lys Thr Ser Asp  
690 695 700

Ala Phe His Ile Thr Tyr Thr Thr Phe Phe Asp Val Thr Glu Leu Asp  
705 710 715 720

Ala Asn Asn Pro Ala Leu Asp His Tyr Arg Asn Thr Ala Ala Ile Asp  
725 730 735

Trp Thr Asp Glu Ala Gly Asn Asn His His Ser Glu Asp Ser Lys Pro  
740 745 750

Phe Lys Pro Leu Pro Ala Phe Asp Leu Asn Ala Gln Lys Ser Gly Val  
755 760 765

Tyr Asn Ala Val Thr Lys Glu Ile Thr Trp Thr Ile Ala Val Asn Leu  
770 775 780

Ser Asn Asn Arg Leu Val Asp Ala Phe Leu Thr Asp Pro Ile Leu Thr  
785 790 795 800

Asn Gln Thr Tyr Leu Ala Gly Ser Leu Lys Val Tyr Glu Gly Asn Thr  
805 810 815

Lys Pro Asp Gly Ser Val Glu Lys Val Lys Pro Thr Gln Pro Leu Thr  
820 825 830

Asp Ile Thr Met Glu Glu Pro Ser Glu Lys Asn Gln Asn Thr Trp Arg  
835 840 845

Val Asp Phe Pro Asn Asp Ser Arg Thr Tyr Val Ile Glu Phe Lys Thr  
850 855 860

Ser Val Asp Glu Lys Val Ile Glu Gly Ser Ala Ser Tyr Asp Asn Thr  
865 870 875 880

Ala Ser Tyr Thr Asn Gln Gly Ser Ser Arg Asp Val Thr Gly Lys Val  
885 890 895

Ser Ile Gln His Gly Gly Glu Ser Val Lys Lys Gly Gly Glu Tyr His  
900 905 910

Lys Asp Asp Pro Asp His Val Tyr Trp His Val Met Ile Asn Gly Ala  
915 920 925

Gln Ser Val Leu Asp Asp Val Val Ile Thr Asp Thr Pro Ser Pro Asn  
930 935 940

Gln Val Leu Asp Pro Glu Ser Leu Val Ile Tyr Gly Thr Asn Val Thr  
945 950 955 960

Glu Asp Gly Thr Ile Thr Pro Asp Lys Ser Val Ile Leu Glu Glu Gly  
965 970 975

Lys Asp Tyr Thr Leu Glu Val Thr Thr Asp Asn Glu Thr Gly Gln Gln  
980 985 990

Lys Ile Val Val Lys Met Ala His Ile Glu Ala Pro Tyr Tyr Met Glu  
995 1000 1005

Tyr Arg Ser Leu Val Thr Ser Ser Ala Ala Gly Ser Thr Asp Thr  
1010 1015 1020

Val Ser Asn Gln Val Ser Ile Thr Gly Asn Gly Ser Glu Val Val  
1025 1030 1035

His Gly Asp Asp Asn Gly Asp Val Val Val Asp Ile Asp His Ser  
1040 1045 1050

Gly Gly His Ala Thr Gly Thr Lys Gly Lys Ile Gln Leu Lys Lys  
1055 1060 1065

Thr Ala Met Asp Glu Thr Thr Ile Leu Ala Gly Ala His Phe Gln  
1070 1075 1080

Ile Trp Asp Gln Ala Lys Thr Gln Val Leu Arg Glu Gly Thr Val  
1085 1090 1095

Asp Ala Thr Gly Val Ile Thr Phe Gly Gly  
1100 1105

<210> 5  
<211> 999  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 5

Glu Glu Ile Thr Asp Leu Phe Leu Gln Lys Glu Val Thr Tyr Ser Gly  
1 5 10 15

Val Glu Gly Gly Lys Ile Gly Glu Asn Trp Lys Tyr Pro Gln Phe Val  
20 25 30

Gly Glu Lys Ala Val Asp Gly Asp Glu Thr Thr Arg Trp Ser Ala Asp  
35 40 45

Lys Gln Asp Glu Gln Trp Leu Ile Val Asp Leu Gly Glu Val Lys Asn  
50 55 60

Ile Gly Glu Leu Val Leu Gln Leu His Ala Glu Ser Pro Val Tyr Glu  
65 70 75 80

Ile Leu Val Ser Thr Asp Gly Glu Ser Tyr Gln Ser Ile Phe Lys Glu  
85 90 95

Glu Asn Gly Lys Gly Gln Pro Thr Lys Lys Tyr Ile Asp Gly Asn  
100 105 110

Asn Val Gln Ala Arg Phe Val Lys Tyr Gln Gln Met Lys Met Trp Gln  
115 120 125

His Thr Asn Lys Gln Phe Tyr Ser Ser Ser Ile Ile Ser Phe Glu Ala  
130 135 140

Tyr Glu Lys Lys Arg Leu Pro Glu Ala Ile Lys Leu Leu Thr Glu Asn  
145 150 155 160

Leu Thr Ile Ser Glu Lys Arg Lys Gln Gln Leu Ala Phe Glu Val Ser  
165 170 175

Pro Ala Gly Val Asp Ile Thr Glu Asp Gln Ile Glu Trp Ser Ser Ser  
180 185 190

Asp Pro Thr Ile Val Thr Val Asp Gln Thr Gly Asn Leu Thr Ala Val  
195 200 205

Lys Ser Gly Glu Ala Lys Val Thr Val Lys Ile Lys Gly Thr Glu Ile  
210 215 220

Ser Asp Thr Ile Pro Val Thr Val Val Ala Glu Asn Lys Gln Tyr Ala  
225 230 235 240

Glu Met Arg Ala Lys Trp Lys Met Arg Leu Leu Gly Thr Thr Gln Tyr  
245 250 255

Asp Asn Asp Ala Asp Val Gln Gln Tyr Arg Ala Gln Ile Ala Thr Glu  
260 265 270

Ser Leu Ala Leu Trp Gln Thr Leu Asn Gln Ala Ala Asp Arg Glu Tyr  
275 280 285

Leu Trp Glu Arg Lys Pro Ser Asp Thr Val Ser Ala Asp Tyr Thr Thr  
290 295 300

Gln Phe Thr Asn Ile Lys Lys Leu Ala Leu Gly Tyr Tyr Glu Pro Ser  
305 310 315 320

Ser Glu Leu Phe Glu Lys Pro Glu Val Tyr Asp Ala Ile Val Lys Gly  
325 330 335

Ile Glu Phe Met Ile Asp Thr Lys Lys Tyr Asn Gly Thr Tyr Tyr Thr  
340 345 350

Gly Asn Trp Trp Asp Trp Gln Ile Gly Ser Ala Gln Pro Leu Thr Asp  
355 360 365

Thr Leu Ile Leu Leu His Asp Asp Leu Leu Asn Thr Asp Ala Glu Lys  
370 375 380

Leu Asn Lys Phe Thr Ala Pro Leu Met Leu Tyr Ala Lys Asp Pro Asn  
385 390 395 400

Ile Gln Trp Pro Ile Tyr Arg Ala Thr Gly Ala Asn Leu Thr Asp Ile  
405 410 415

Ser Ile Thr Val Leu Gly Thr Gly Leu Leu Leu Glu Asp Asn Gln Arg  
420 425 430

Leu Val Gln Val Gln Glu Ala Val Pro Ser Val Leu Lys Ser Val Ser  
435 440 445

Ser Gly Asp Gly Leu Tyr Pro Asp Gly Ser Leu Ile Gln His Gly Tyr  
450 455 460

Phe Pro Tyr Asn Gly Ser Tyr Gly Asn Glu Leu Leu Lys Gly Phe Gly  
465 470 475 480

Arg Ile Gln Thr Ile Leu Gln Gly Ser Asp Trp Glu Met Asn Asp Pro  
485 490 495

Asn Ile Ser Asn Leu Phe Asn Val Val Asp Lys Gly Tyr Leu Gln Leu  
500 505 510

Met Val Asn Gly Lys Met Pro Ser Met Val Ser Gly Arg Ser Ile Ser  
515 520 525

Arg Ala Pro Glu Thr Asn Pro Phe Thr Thr Glu Phe Glu Ser Gly Lys  
530 535 540

Glu Thr Ile Ala Asn Leu Thr Leu Ile Ala Lys Phe Ala Pro Glu Asn  
545 550 555 560

Leu Arg Asn Asp Ile Tyr Thr Ser Ile Gln Thr Trp Leu Gln Gln Ser  
565 570 575

Gly Ser Tyr Tyr His Phe Phe Lys Lys Pro Arg Asp Phe Glu Ala Leu  
580 585 590

Ile Asp Leu Lys Asn Val Val Asn Ser Ala Ser Pro Ala Gln Ala Thr  
595 600 605

Pro Met Gln Ser Leu Asn Val Tyr Gly Ser Met Asp Arg Val Leu Gln  
610 615 620

Lys Asn Asn Glu Tyr Ala Val Gly Ile Ser Met Tyr Ser Gln Arg Val  
625 630 635 640

Gly Asn Tyr Glu Phe Gly Asn Thr Glu Asn Lys Lys Gly Trp His Thr  
645 650 655

Ala Asp Gly Met Leu Tyr Leu Tyr Asn Gln Asp Phe Ala Gln Phe Asp  
660 665 670

Glu Gly Tyr Trp Ala Thr Ile Asp Pro Tyr Arg Leu Pro Gly Thr Thr  
675 680 685

Val Asp Thr Arg Glu Leu Ala Asn Gly Ala Tyr Thr Gly Lys Arg Ser

690

695

700

Pro Gln Ser Trp Val Gly Gly Ser Asn Asn Gly Gln Val Ala Ser Ile  
705 710 715 720

Gly Met Phe Leu Asp Lys Ser Asn Glu Gly Met Asn Leu Val Ala Lys  
725 730 735

Lys Ser Trp Phe Leu Leu Asp Gly Gln Ile Ile Asn Leu Gly Ser Gly  
740 745 750

Ile Thr Gly Thr Thr Asp Ala Ser Ile Glu Thr Ile Leu Asp Asn Arg  
755 760 765

Met Ile His Pro Gln Glu Val Lys Leu Asn Gln Gly Ser Asp Lys Asp  
770 775 780

Asn Ser Trp Ile Ser Leu Ser Ala Ala Asn Pro Leu Asn Asn Ile Gly  
785 790 795 800

Tyr Val Phe Pro Asn Ser Met Asn Thr Leu Asp Val Gln Ile Glu Glu  
805 810 815

Arg Ser Gly Arg Tyr Gly Asp Ile Asn Glu Tyr Phe Val Asn Asp Lys  
820 825 830

Thr Tyr Thr Asn Thr Phe Ala Lys Ile Ser Lys Asn Tyr Gly Lys Thr  
835 840 845

Val Glu Asn Gly Thr Tyr Glu Tyr Leu Thr Val Val Gly Lys Thr Asn  
850 855 860

Glu Glu Ile Ala Ala Leu Ser Lys Asn Lys Gly Tyr Thr Val Leu Glu  
865 870 875 880

Asn Thr Ala Asn Leu Gln Ala Ile Glu Ala Gly Asn Tyr Val Met Met  
885 890 895

Asn Thr Trp Asn Asn Asp Gln Glu Ile Ala Gly Leu Tyr Ala Tyr Asp  
900 905 910

Pro Met Ser Val Ile Ser Glu Lys Ile Asp Asn Gly Val Tyr Arg Leu  
915 920 925

Thr Leu Ala Asn Pro Leu Gln Asn Asn Ala Ser Val Ser Ile Glu Phe  
930 935 940

Asp Lys Gly Ile Leu Glu Val Val Ala Ala Asp Pro Glu Ile Ser Val  
945 950 955 960

Asp Gln Asn Ile Ile Thr Leu Asn Ser Ala Gly Leu Asn Gly Ser Ser  
965 970 975

Arg Ser Ile Ile Val Lys Thr Thr Pro Glu Val Thr Lys Glu Ala Leu  
980 985 990

Glu Lys Leu Ile Gln Glu Gln  
995

<210> 6  
<211> 741  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 6

Gln Glu Val Thr Ser Asp Ala Glu Lys Thr Val Glu Lys Asp Gly Leu  
1 5 10 15

Lys Val Ile Gly Lys Ile Glu Asp Thr Ser Ser Gln Glu Asp Ile Lys  
20 25 30

Thr Val Thr Tyr Glu Val Thr Asn Thr Arg Asp Val Pro Ile Lys Asp  
35 40 45

Leu Ile Leu Lys Gln Lys Asn Thr Asn Asp Ser Pro Ile Lys Phe Val  
50 55 60

Leu Asp Thr Leu Ser Glu Glu Arg Gly Pro Thr Ser Leu Glu Glu Gln  
65 70 75 80

Ala Lys Val Glu Thr Asn Glu Lys Asp Gln Thr Thr Asp Ile Lys Leu  
85 90 95

Leu Asn Leu Gln Pro Asn Ser Thr Arg Lys Ile Thr Ile Asn Gly Gln  
100 105 110

Ile Thr Thr Lys Ala Ser Asn Lys Leu Leu Val Ser Val Leu Ile Glu  
115 120 125

Asp Asn Glu Lys Gly Thr Leu Val Ile Asp Leu Pro Ser Lys Asp Ile  
130 135 140

Leu Ala Asp Lys Glu Ser Val Ser Lys Glu Lys Gln Glu Thr Ser Glu  
145 150 155 160

Thr Lys Val Glu Asn Gln Ala Asn Glu Thr Ala Ser Ser Thr Asn Glu  
165 170 175

Met Thr Ala Thr Thr Ser Asn Glu Thr Lys Pro Glu Ala Gly Lys Ala  
180 185 190

Ile Glu Ser Ile Gln Glu Thr Ala Leu Thr Gln Ala Thr Glu Ser Pro  
195 200 205

Glu Gln Pro Pro Leu Lys Ala Gln Pro Thr Gly Pro Leu Val Pro Pro  
210 215 220

Thr Pro Gly Arg Gly Phe Asn Thr Pro Ile Tyr Gln Ser Val His Lys  
225 230 235 240

Gly Glu Leu Phe Ser Thr Gly Asn Thr Asn Leu Lys Ile Ala Asn Glu  
245 250 255

Asn Thr Ala Ala Ala Gln Thr Phe Leu Asn Thr Arg Gly Ala Ser Ser  
260 265 270

Gly Tyr Ala Ile Asn Asn Phe Pro Leu Glu Phe Ala Asp Val Asp Asn  
275 280 285

Asp Pro Asn Thr Tyr Asn Ser Ser Arg Ala Tyr Ile Asp Leu Asn Gly  
290 295 300

Ala Lys Glu Ile Ala Trp Ala Gly Leu Phe Trp Ser Ala Ser Arg Tyr  
305 310 315 320

Lys Gly Pro Ala Tyr Gly Thr Asn Leu Ser Asp Glu Glu Ile Ser Ala  
325 330 335

Pro Val Gln Phe Thr Thr Pro Asn Gly Thr Val Gln Arg Val Ser Pro

340

345

350

Gln Arg Tyr His Arg Ile Asp Gln Asp Ala Thr Asn Pro Gly Gln Arg  
355 360 365

Phe Gly Tyr Asn Asn Thr Gly Phe Ser Asn Tyr Ala Asp Val Thr Ser  
370 375 380

Ile Leu Gln Gly Asp Lys Ser Ala Thr Gly Ser Tyr Thr Leu Ala Asp  
385 390 395 400

Ile Pro Met Thr Ser Ser Leu Asn Gly Gln Tyr Gln Tyr Tyr Asn Phe  
405 410 415

Ser Gly Trp Ser Leu Phe Val Val Thr Lys Asp Gln Ala Ser Lys Ser  
420 425 430

Arg Ala Phe Ser Ile Tyr Tyr Gly Ala Arg Gly Asn Ala Ala Gly Thr  
435 440 445

Asn Asn Glu Phe Thr Met Ser Asn Phe Leu Thr Ala Lys Gln Gly Asn  
450 455 460

Leu Asp Pro Ile Val Thr Trp Phe Thr Val Gln Gly Asp Lys Tyr Trp  
465 470 475 480

Thr Gly Asp Asn Ala Gln Ile Lys Asn Ser Ala Gly Thr Trp Val Asn  
485 490 495

Ile Ser Asn Thr Leu Asn Pro Val Asn Asn Ala Met Asn Ala Thr Val  
500 505 510

Thr Asp Asn Asp Glu His Met Val Asp Lys Tyr Pro Gly Lys Phe Ala  
515 520 525

Pro Asp His Pro Asn Phe Leu Asp Ile Asp Ile Asp Arg Met Ala Ile  
530 535 540

Pro Glu Gly Val Leu Asn Ala Gly Gln Asn Gln Ile Asn Phe Arg Thr  
545 550 555 560

Thr Ser Ser Gly Asp Asp Tyr Ser Thr Asn Ala Ile Gly Phe Ala Val  
565 570 575

Asn Ala Glu Thr Pro Glu Phe Glu Ile Lys Lys Glu Ile Val Glu Pro  
580 585 590

Lys Glu Thr Tyr Lys Val Gly Glu Thr Ile Thr Tyr Arg Val Ser Leu  
595 600 605

Lys Asn Thr Lys Ala Asp Ser Glu Ala Ile Asn Ser Val Ser Lys Asp  
610 615 620

Ala Leu Asp Gly Arg Leu Asn Tyr Leu Pro Gly Ser Leu Lys Ile Ile  
625 630 635 640

Ser Gly Pro Asn Ser Gly Glu Lys Thr Asp Ala Ser Gly Asp Asp Gln  
645 650 655

Ala Glu Tyr Asp Glu Thr Asn Lys Gln Ile Ile Val Arg Val Gly Asn  
660 665 670

Gly Ala Thr Ala Thr Gln Gly Gly Ser Tyr Lys Ala Asp Thr Ala Glu  
675 680 685

Thr Ile Tyr Glu Phe Lys Ala Arg Ile Asn Glu Arg Ala Lys Ala Asn  
690 695 700

Glu Leu Val Pro Asn Ser Ala Thr Val Glu Ala Val Asp Ile Leu Thr  
705 710 715 720

Ser Ala Lys Val Asn Glu Thr Ser Asn Ile Val Glu Ala Lys Ile Ala  
725 730 735

Asp Glu Gln Val Thr  
740

<210> 7  
<211> 570  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 7

Glu Thr Gly Tyr Ala Gln Thr Glu Pro Thr Ser Thr Ser Glu Thr Asn  
1 5 10 15

Gln Ile Ser Ala Thr Pro Asn Val Val Pro Arg Lys Gln Val Gly Asn  
20 25 30

Ile Val Thr Ala Ile Gln Leu Thr Asp Lys Glu Gly Asn Pro Leu Gly  
35 40 45

Thr Ile Asn Gln Tyr Thr Asp Ile Tyr Leu Arg Ile Glu Phe Asn Leu  
50 55 60

Pro Asp Asn Thr Val Asn Ser Gly Asp Thr Ser Val Ile Thr Leu Pro  
65 70 75 80

Glu Glu Leu Arg Leu Glu Lys Asn Met Thr Phe Asn Val Val Asp Asp  
85 90 95

Thr Gly Thr Val Val Ala Ile Ala Gln Thr Asp Val Ala Asn Lys Thr  
100 105 110

Val Thr Leu Thr Tyr Thr Asp Tyr Val Glu Asn His Ala Asn Ile Ser  
115 120 125

Gly Ser Leu Tyr Phe Thr Ser Leu Ile Asp Phe Glu Asn Val Glu Asn  
130 135 140

Glu Ser Lys Ile Pro Ile Tyr Val Thr Val Glu Gly Glu Lys Ile Phe  
145 150 155 160

Ala Gly Asp Leu Asp Tyr Gln Gly Glu Gly Asp Asp Val Asn Glu Lys  
165 170 175

Phe Ser Lys Tyr Ser Trp Phe Ile Glu Asp Asp Pro Thr Glu Ile Tyr  
180 185 190

Asn Val Leu Arg Ile Asn Pro Thr Gly Gln Thr Tyr Thr Asp Leu Glu  
195 200 205

Val Glu Asp Val Leu Lys Thr Glu Ser Leu Ser Tyr Met Lys Asp Thr  
210 215 220

Met Lys Ile Glu Arg Gly Gln Trp Thr Leu Asp Gly Asn Ala Ile Trp  
225 230 235 240

Gln Phe Thr Pro Glu Glu Asp Ile Thr Asp Gln Leu Ala Val Gln Tyr

245

250

255

Gly Pro Asp Asp Arg Asn Phe Ser Val His Phe Gly Asn Ile Gly Thr  
260 265 270

Asn Glu Tyr Arg Ile Thr Tyr Lys Thr Lys Ile Asp His Leu Pro Glu  
275 280 285

Lys Gly Glu Thr Phe Thr Asn Tyr Ala Lys Leu Thr Glu Asn Gln Thr  
290 295 300

Val Val Glu Glu Val Glu Val Ser Arg Val Ser Gln Thr Gly Gly  
305 310 315 320

Glu Ala Asn Gly Glu Gln Tyr Val Val Glu Ile His Lys Glu Asp Glu  
325 330 335

Ala Gly Gln Arg Leu Ala Gly Ala Glu Phe Glu Leu Ile Arg Asn Ser  
340 345 350

Thr Asn Gln Thr Val Ala Lys Ile Thr Thr Asp Gln Asn Gly Thr Ala  
355 360 365

Ile Val Lys Gly Leu Leu Lys Asp Asn Tyr Thr Leu Val Glu Thr Lys  
370 375 380

Ala Pro Thr Gly Tyr Gln Leu Ser Gln Asn Lys Ile Pro Ile Thr Pro  
385 390 395 400

Glu Asp Phe Gly Lys Asn Leu Val Ala Leu Lys Thr Val Val Asn His  
405 410 415

Lys Ile Ser Tyr Gln Pro Val Ala Ala Ser Phe Leu Ala Gly Lys Val  
420 425 430

Leu Leu Gly Lys Pro Leu Lys Asp Ala Glu Phe Gln Phe Glu Leu Leu  
435 440 445

Asp Glu Lys Gly Thr Val Leu Glu Thr Val Ser Asn Asp Thr Leu Gly  
450 455 460

Lys Ile Gln Phe Ser Pro Leu Thr Phe Glu Thr Pro Gly Asn Tyr Gln  
465 470 475 480

Tyr Thr Ile Arg Glu Val Asn Thr Gln Gln Thr Gly Val Ser Tyr Asp  
485 490 495

Thr His Asn Leu Gln Val Gln Val Thr Val Glu Ala Leu Leu Gly Asn  
500 505 510

Leu Val Ala Thr Thr Gln Tyr Asp Gly Gly Gln Val Phe Thr Asn His  
515 520 525

Tyr Thr Pro Glu Lys Pro Ile Glu Ser Thr Thr Pro Pro Thr Ser Gly  
530 535 540

Thr Thr Asp Thr Thr Asn Ser Thr Thr Glu Thr Thr Ser Ile Thr  
545 550 555 560

Ile Glu Lys Gln Ala Ile Arg Asn Lys Glu  
565 570

<210> 8  
<211> 3309  
<212> DNA  
<213> *Staphylococcus epidermidis*

<400> 8  
atgataaacag atgagaatga taaaacgaat attaatatcg agttaaatct tctcaaccaa 60  
acagagcagc cattacaacg agaaattcaa ttgaaaaatg cacagttcat ggatactgct 120  
gtaattgaaa aagacggata ttcttaccaa gtgactaatg gtacgcttta tctgactttg 180  
gacgcacaag taaaaaagcc ggtacagctt tcgttagctg ttgagcaaag ttgcgttcaa 240  
acagctcagc cacctaagtt attgtatgaa aacaacgaat atgatgttc agttaacttct 300  
gaaaaaataa cagtagagga ttctgctaaa gaatcaactg aaccagaaaa aataactgta 360  
ccagaaaata cgaaagaaac taacaaaaat gattcggctc cagaaaaaac agaacagccg 420  
accgcaacag aagaggtaac caatccattt gcagaagcaa gaatggcgcc agctactttg 480  
agagcgaatc tggcactgcc tttaattgca ccacaataca cgacggataa ttctggact 540  
tatccgacag ctaattggca gcccacagggc aatcaaaatg tggtaaacca tcaaggaaat 600  
aaagacggta gtgcacaatg ggacggccaa acgagttgga atggggaccc tactaatcgc 660  
acaaattctt atattgagta tggcggtaca ggagaccaag ccgattatgc catccaaaaa 720  
tatgctagag aaacaacaac accaggcctt tttgatgtat atcttaatgt gcgtggaaat 780

gttcagaaag aaatcacgcc attggatttg gtcttagtcg ttgactggc cggtatgtatg 840  
aatgaaaaca atcggattgg tgaagttcaa aaaggagtga accgtttgt tgatacattg 900  
gcagatagcg gtattaccaa taacatcaac atggctatg ttggctactc aagtgacggt 960  
tataataaca acgccattca aatggggccg tttgatacag tcaaaaatcc aattaaaaat 1020  
attacgccaa gtagcactag aggaggaact ttcactcaaa aagcattaag agatgctggt 1080  
gataatgttag caacgccaaa tggacataag aaagtcatgt tacttttaac ggtatggcg 1140  
ccaaaccccttct cttataaaagt gagtcgagtt caaacagagg cgatggtcg cttttacggg 1200  
acacaattta cgaatcgaca agatcaacca ggtacactt cttatatctc tggtagctat 1260  
aatgcgccag atcaaaaacaa tatcaataaa cggattaaca gtacgtttat cgccacgata 1320  
ggtagggcaa tggctttaaa acaacgtggg attgaaatac atggattggg cattcaattt 1380  
caaagcgatc cacgagctaa ttatctaaa caacaagttt aagataaaat gcgtgagatg 1440  
gtgtcagccg atgaaaatgg agacctttat tatgaatccg cggattatgc accagacatt 1500  
tctgatttatt tagcgaaaaa agccgttcag atttcaggaa cggttgtaaa cgaaaaagta 1560  
gttgatccaa ttgctgaacc ttttaatac gagccaaata cattatcaat gaaaagtgt 1620  
ggtcctgttc aggttcaaac attaccagaa gtgtcgctaa caggcgctac aattaatagt 1680  
aatgagattt atttggtaa agggcaagaa attcaaattt attatcaagt acgtattcaa 1740  
acagagtcag aaaacttcaa acctgatttt tggtatcaaa tgaatggtcg gacaacgttt 1800  
cagccattag ccacggcccc tggaaaaagtt gatttgggg ttccttcggg aaaagcacct 1860  
ggcgtgaagt taaacgtgaa aaaaatctgg gaagagtatg atcaagaccc gacaagtcgg 1920  
ccagataatg tgatttatga aatttagtaga aagcaagttt ctgacacagc caactggcaa 1980  
actgggtata ttaaatttac aaaaccagaa aatgatacca gcaatagttt ggagcgcaaa 2040  
aatgtaaaccc aactttccaa aaccgcggat gaaagctatc aagaagttt tgggcttccc 2100  
caatacaaca atcaaggaca agctttcaat tatcaaacaa cccgtgaatt agcagttcct 2160  
ggttacagtc aagaaaaat cgacgatact acttggaaaa acacgaagca gttcaagcc 2220  
tttagatttaa aagtaatcaa aaattcttcc tcaggtgaga aaaacttagt gggagccgtc 2280  
tttgaattga gtggtaaaaa tggtaaaca acattagtgg acaataaaga tggtagctat 2340  
tccttgccaa aagatgtgct cctacaaaaa ggggaacgct atacattaaac tgaagtaaaa 2400  
gcacctgcag gacatgagtt aggcaagaaa acgacttggc aaattgaggt gagtgagcaa 2460

ggcaaagtaa gcatcgatgg acaagaagtg accaccacaa atcaagttat tccattggaa	2520
attgaaaata aattttcttc tttgccaatc agaatttagaa aatacaccat gcaaaatggc	2580
aaacaagtga acttagcaga ggcgactttt gcgttgc当地 gaaaaatgc tcaaggaagt	2640
taccaaactg tggcaactca aaaaacagat actacaggat tgagctattt taaaatttagt	2700
gaacctggtg agtacgat ggtggAACAA tcaggaccat taggctacga cactcttgct	2760
ggaaattatg aatttactgt tgataaatat gggaaaattc actatgcagg caaaaatatt	2820
gaagaaaaatg cgccagaatg gacactgaca catcaaaata atttgaaacc ttttgactta	2880
acagttata aaaaagccga taatcagacg ccactaaag gagcgaattt ccgttaaca	2940
ggaccagata cggatattga attacaaaaa gatggcaaag aaacggatac ttttgaaaa	3000
gaaaacttaa aaccaggaa atatgttcta acagaaacct ttacgccaga aggatatcag	3060
gggttaaaag aaccaatcga attaataatt cgtgaagatg gttcagtcac gatagatggg	3120
gaaaaagtag cagatgtttt aatttctgga gagaagaata atcaaattac ttttagacgtt	3180
acgaaccaag caaaggttcc ttacctgaa actggggca taggacgctt gtggtttac	3240
ttgatagcga ttagtacatt cgtgatagcg ggtgtttatc tctttattag acgaccagaa	3300
gggagtgtg	3309

<210> 9  
 <211> 1103  
 <212> PRT  
 <213> *Staphylococcus epidermidis*

<400> 9

Met Ile Thr Asp Glu Asn Asp Lys Thr Asn Ile Asn Ile Glu Leu Asn	
1	5
10	15

Leu Leu Asn Gln Thr Glu Gln Pro Leu Gln Arg Glu Ile Gln Leu Lys	
20	25
30	

Asn Ala Gln Phe Met Asp Thr Ala Val Ile Glu Lys Asp Gly Tyr Ser	
35	40
45	

Tyr Gln Val Thr Asn Gly Thr Leu Tyr Leu Thr Leu Asp Ala Gln Val	
50	55
60	

Lys Lys Pro Val Gln Leu Ser Leu Ala Val Glu Gln Ser Ser Leu Gln	
65	70
75	80

Thr Ala Gln Pro Pro Lys Leu Leu Tyr Glu Asn Asn Glu Tyr Asp Val  
85 90 95

Ser Val Thr Ser Glu Lys Ile Thr Val Glu Asp Ser Ala Lys Glu Ser  
100 105 110

Thr Glu Pro Glu Lys Ile Thr Val Pro Glu Asn Thr Lys Glu Thr Asn  
115 120 125

Lys Asn Asp Ser Ala Pro Glu Lys Thr Glu Gln Pro Thr Ala Thr Glu  
130 135 140

Glu Val Thr Asn Pro Phe Ala Glu Ala Arg Met Ala Pro Ala Thr Leu  
145 150 155 160

Arg Ala Asn Leu Ala Leu Pro Leu Ile Ala Pro Gln Tyr Thr Thr Asp  
165 170 175

Asn Ser Gly Thr Tyr Pro Thr Ala Asn Trp Gln Pro Thr Gly Asn Gln  
180 185 190

Asn Val Leu Asn His Gln Gly Asn Lys Asp Gly Ser Ala Gln Trp Asp  
195 200 205

Gly Gln Thr Ser Trp Asn Gly Asp Pro Thr Asn Arg Thr Asn Ser Tyr  
210 215 220

Ile Glu Tyr Gly Gly Thr Gly Asp Gln Ala Asp Tyr Ala Ile Arg Lys  
225 230 235 240

Tyr Ala Arg Glu Thr Thr Pro Gly Leu Phe Asp Val Tyr Leu Asn  
245 250 255

Val Arg Gly Asn Val Gln Lys Glu Ile Thr Pro Leu Asp Leu Val Leu  
260 265 270

Val Val Asp Trp Ser Gly Ser Met Asn Glu Asn Asn Arg Ile Gly Glu  
275 280 285

Val Gln Lys Gly Val Asn Arg Phe Val Asp Thr Leu Ala Asp Ser Gly  
290 295 300

Ile Thr Asn Asn Ile Asn Met Gly Tyr Val Gly Tyr Ser Ser Asp Gly  
305 310 315 320

Tyr Asn Asn Asn Ala Ile Gln Met Gly Pro Phe Asp Thr Val Lys Asn  
325 330 335

Pro Ile Lys Asn Ile Thr Pro Ser Ser Thr Arg Gly Gly Thr Phe Thr  
340 345 350

Gln Lys Ala Leu Arg Asp Ala Gly Asp Met Leu Ala Thr Pro Asn Gly  
355 360 365

His Lys Lys Val Ile Val Leu Leu Thr Asp Gly Val Pro Thr Phe Ser  
370 375 380

Tyr Lys Val Ser Arg Val Gln Thr Glu Ala Asp Gly Arg Phe Tyr Gly  
385 390 395 400

Thr Gln Phe Thr Asn Arg Gln Asp Gln Pro Gly Ser Thr Ser Tyr Ile  
405 410 415

Ser Gly Ser Tyr Asn Ala Pro Asp Gln Asn Asn Ile Asn Lys Arg Ile  
420 425 430

Asn Ser Thr Phe Ile Ala Thr Ile Gly Glu Ala Met Val Leu Lys Gln  
435 440 445

Arg Gly Ile Glu Ile His Gly Leu Gly Ile Gln Leu Gln Ser Asp Pro  
450 455 460

Arg Ala Asn Leu Ser Lys Gln Gln Val Glu Asp Lys Met Arg Glu Met  
465 470 475 480

Val Ser Ala Asp Glu Asn Gly Asp Leu Tyr Tyr Glu Ser Ala Asp Tyr  
485 490 495

Ala Pro Asp Ile Ser Asp Tyr Leu Ala Lys Lys Ala Val Gln Ile Ser  
500 505 510

Gly Thr Val Val Asn Gly Lys Val Val Asp Pro Ile Ala Glu Pro Phe  
515 520 525

Lys Tyr Glu Pro Asn Thr Leu Ser Met Lys Ser Val Gly Pro Val Gln

530

535

540

Val Gln Thr Leu Pro Glu Val Ser Leu Thr Gly Ala Thr Ile Asn Ser  
545 550 555 560

Asn Glu Ile Tyr Leu Gly Lys Gly Gln Glu Ile Gln Ile His Tyr Gln  
565 570 575

Val Arg Ile Gln Thr Glu Ser Glu Asn Phe Lys Pro Asp Phe Trp Tyr  
580 585 590

Gln Met Asn Gly Arg Thr Thr Phe Gln Pro Leu Ala Thr Ala Pro Glu  
595 600 605

Lys Val Asp Phe Gly Val Pro Ser Gly Lys Ala Pro Gly Val Lys Leu  
610 615 620

Asn Val Lys Lys Ile Trp Glu Glu Tyr Asp Gln Asp Pro Thr Ser Arg  
625 630 635 640

Pro Asp Asn Val Ile Tyr Glu Ile Ser Arg Lys Gln Val Thr Asp Thr  
645 650 655

Ala Asn Trp Gln Thr Gly Tyr Ile Lys Leu Ser Lys Pro Glu Asn Asp  
660 665 670

Thr Ser Asn Ser Trp Glu Arg Lys Asn Val Thr Gln Leu Ser Lys Thr  
675 680 685

Ala Asp Glu Ser Tyr Gln Glu Val Leu Gly Leu Pro Gln Tyr Asn Asn  
690 695 700

Gln Gly Gln Ala Phe Asn Tyr Gln Thr Thr Arg Glu Leu Ala Val Pro  
705 710 715 720

Gly Tyr Ser Gln Glu Lys Ile Asp Asp Thr Thr Trp Lys Asn Thr Lys  
725 730 735

Gln Phe Lys Pro Leu Asp Leu Lys Val Ile Lys Asn Ser Ser Ser Gly  
740 745 750

Glu Lys Asn Leu Val Gly Ala Val Phe Glu Leu Ser Gly Lys Asn Val  
755 760 765

Gln Thr Thr Leu Val Asp Asn Lys Asp Gly Ser Tyr Ser Leu Pro Lys  
770 775 780

Asp Val Arg Leu Gln Lys Gly Glu Arg Tyr Thr Leu Thr Glu Val Lys  
785 790 795 800

Ala Pro Ala Gly His Glu Leu Gly Lys Lys Thr Thr Trp Gln Ile Glu  
805 810 815

Val Ser Glu Gln Gly Lys Val Ser Ile Asp Gly Gln Glu Val Thr Thr  
820 825 830

Thr Asn Gln Val Ile Pro Leu Glu Ile Glu Asn Lys Phe Ser Ser Leu  
835 840 845

Pro Ile Arg Ile Arg Lys Tyr Thr Met Gln Asn Gly Lys Gln Val Asn  
850 855 860

Leu Ala Glu Ala Thr Phe Ala Leu Gln Arg Lys Asn Ala Gln Gly Ser  
865 870 875 880

Tyr Gln Thr Val Ala Thr Gln Lys Thr Asp Thr Thr Gly Leu Ser Tyr  
885 890 895

Phe Lys Ile Ser Glu Pro Gly Glu Tyr Arg Met Val Glu Gln Ser Gly  
900 905 910

Pro Leu Gly Tyr Asp Thr Leu Ala Gly Asn Tyr Glu Phe Thr Val Asp  
915 920 925

Lys Tyr Gly Lys Ile His Tyr Ala Gly Lys Asn Ile Glu Glu Asn Ala  
930 935 940

Pro Glu Trp Thr Leu Thr His Gln Asn Asn Leu Lys Pro Phe Asp Leu  
945 950 955 960

Thr Val Asn Lys Lys Ala Asp Asn Gln Thr Pro Leu Lys Gly Ala Lys  
965 970 975

Phe Arg Leu Thr Gly Pro Asp Thr Asp Ile Glu Leu Pro Lys Asp Gly  
980 985 990

Lys Glu Thr Asp Thr Phe Val Phe Glu Asn Leu Lys Pro Gly Lys Tyr  
995 1000 1005

Val Leu Thr Glu Thr Phe Thr Pro Glu Gly Tyr Gln Gly Leu Lys  
1010 1015 1020

Glu Pro Ile Glu Leu Ile Ile Arg Glu Asp Gly Ser Val Thr Ile  
1025 1030 1035

Asp Gly Glu Lys Val Ala Asp Val Leu Ile Ser Gly Glu Lys Asn  
1040 1045 1050

Asn Gln Ile Thr Leu Asp Val Thr Asn Gln Ala Lys Val Pro Leu  
1055 1060 1065

Pro Glu Thr Gly Gly Ile Gly Arg Leu Trp Phe Tyr Leu Ile Ala  
1070 1075 1080

Ile Ser Thr Phe Val Ile Ala Gly Val Tyr Leu Phe Ile Arg Arg  
1085 1090 1095

Pro Glu Gly Ser Val  
1100

<210> 10

<211> 1428

<212> DNA

<213> Staphylococcus epidermidis

<400> 10  
atgaaaaaacg cacgttggtt aagtatttgc gtcatgctac tcgcttttt cgggtttca 60  
cagcaagcat tagcagaggc atcgcaagca agcggtcaag ttacgttgca caaattattg 120  
ttccctgatg gtcaattacc agaacagcag caaaacacag gggaaagaggg aacgctgctt 180  
caaaattatc ggggcttaaa tgacgtcact tatcaagtct atgatgtgac ggatccgttt 240  
tatcagcttc gttctgaagg aaaaacggtc caagaggcac agcgtcaatt agcagaaacc 300  
ggtgcaacaa atagaaaacc gatcgccagaa gataaaacac agacaataaa tggagaagat 360  
ggagtggttt cttttcatt agcttagcaaa gattcgcagc aacgagataa agccttattt 420  
tttggtaag cggaagcacc agaagtggta aaggaaaaag ctagcaacct agtagtgatt 480  
ttgcctgttc aagatccaca agggcaatcg ttaacgcata ttcatttata tccaaaaat 540

gaagaaaaatg cctatgactt accaccactt gaaaaaacgg tactcgataa gcaacaaggc	600
tttaatcaag gagagcacat taactatcag ttaacgactc agattccagc gaatatttt	660
ggatatcagg aattccgtt gtcagataag gcggatacaa cgttgacact tttaccagaa	720
tcaattgagg taaaagtggc tggaaaaaca gttactacag gttacacact gacgacgcaa	780
aagcatggat ttacgcttga ttttcaatt aaagacttac aaaactttgc aaatcaaaca	840
atgactgtgt cgtatcaaat gcgttagaa aagaccgctg aacctgacac tgcgattaac	900
aacgaaggac aattagtac ggacaaacat accttgacta aaagagccac agttcgtaca	960
ggcggcaagt cttttgtcaa agttgatagt gaaaatgcga aaatcacctt gccagaggct	1020
tggcaaaaag aaaaagcatt agctaaaaaa ttcacgtcta atcaagccgg tgaattttca	1080
gttaaaggct taaaagatgg ccagtttttc ttggaaagaaa tctctgcacc aaaaggttat	1140
cttctgaatc aaacagaaat tcctttacg gtggaaaaaa attcttatgc aacgaacgga	1200
caacgaacag caccgttaca tgtaatcaat aaaaaagtaa aagagtcaagg cttcttacca	1260
aaaacaaatg aagaacgttc tatttggttg acgattgcag gcctgctaattt cattggatg	1320
gtagtcattt ggctatttta tcaaaaacaa aaaagaggag agagaaaa	1380
	1428

<210> 11

<211> 476

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 11

Met Lys Asn Ala Arg Trp Leu Ser Ile Cys Val Met Leu Leu Ala Leu			
1	5	10	15
10	15		

Phe Gly Phe Ser Gln Gln Ala Leu Ala Glu Ala Ser Gln Ala Ser Val			
20	25	30	
30			

Gln Val Thr Leu His Lys Leu Leu Phe Pro Asp Gly Gln Leu Pro Glu			
35	40	45	
45			

Gln Gln Gln Asn Thr Gly Glu Glu Gly Thr Leu Leu Gln Asn Tyr Arg			
50	55	60	
60			

Gly Leu Asn Asp Val Thr Tyr Gln Val Tyr Asp Val Thr Asp Pro Phe			
65	70	75	80
75	80		

Tyr Gln Leu Arg Ser Glu Gly Lys Thr Val Gln Glu Ala Gln Arg Gln  
85 90 95

Leu Ala Glu Thr Gly Ala Thr Asn Arg Lys Pro Ile Ala Glu Asp Lys  
100 105 110

Thr Gln Thr Ile Asn Gly Glu Asp Gly Val Val Ser Phe Ser Leu Ala  
115 120 125

Ser Lys Asp Ser Gln Gln Arg Asp Lys Ala Tyr Leu Phe Val Glu Ala  
130 135 140

Glu Ala Pro Glu Val Val Lys Glu Lys Ala Ser Asn Leu Val Val Ile  
145 150 155 160

Leu Pro Val Gln Asp Pro Gln Gly Gln Ser Leu Thr His Ile His Leu  
165 170 175

Tyr Pro Lys Asn Glu Glu Asn Ala Tyr Asp Leu Pro Pro Leu Glu Lys  
180 185 190

Thr Val Leu Asp Lys Gln Gln Gly Phe Asn Gln Gly Glu His Ile Asn  
195 200 205

Tyr Gln Leu Thr Thr Gln Ile Pro Ala Asn Ile Leu Gly Tyr Gln Glu  
210 215 220

Phe Arg Leu Ser Asp Lys Ala Asp Thr Thr Leu Thr Leu Leu Pro Glu  
225 230 235 240

Ser Ile Glu Val Lys Val Ala Gly Lys Thr Val Thr Thr Gly Tyr Thr  
245 250 255

Leu Thr Thr Gln Lys His Gly Phe Thr Leu Asp Phe Ser Ile Lys Asp  
260 265 270

Leu Gln Asn Phe Ala Asn Gln Thr Met Thr Val Ser Tyr Gln Met Arg  
275 280 285

Leu Glu Lys Thr Ala Glu Pro Asp Thr Ala Ile Asn Asn Glu Gly Gln  
290 295 300

Leu Val Thr Asp Lys His Thr Leu Thr Lys Arg Ala Thr Val Arg Thr  
305 310 315 320

Gly Gly Lys Ser Phe Val Lys Val Asp Ser Glu Asn Ala Lys Ile Thr  
325 330 335

Leu Pro Glu Ala Val Phe Ile Val Lys Asn Gln Ala Gly Glu Tyr Leu  
340 345 350

Asn Glu Thr Ala Asn Gly Tyr Arg Trp Gln Lys Glu Lys Ala Leu Ala  
355 360 365

Lys Lys Phe Thr Ser Asn Gln Ala Gly Glu Phe Ser Val Lys Gly Leu  
370 375 380

Lys Asp Gly Gln Tyr Phe Leu Glu Glu Ile Ser Ala Pro Lys Gly Tyr  
385 390 395 400

Leu Leu Asn Gln Thr Glu Ile Pro Phe Thr Val Gly Lys Asn Ser Tyr  
405 410 415

Ala Thr Asn Gly Gln Arg Thr Ala Pro Leu His Val Ile Asn Lys Lys  
420 425 430

Val Lys Glu Ser Gly Phe Leu Pro Lys Thr Asn Glu Glu Arg Ser Ile  
435 440 445

Trp Leu Thr Ile Ala Gly Leu Leu Ile Ile Gly Met Val Val Ile Trp  
450 455 460

Leu Phe Tyr Gln Lys Gln Lys Arg Gly Glu Arg Lys  
465 470 475

<210> 12  
<211> 1881  
<212> DNA  
<213> *Staphylococcus epidermidis*

<400> 12  
atgaagcaat taaaaaaaaagt ttgggtacacc gtttagtacct tgttactaat tttgccactt 60

ttcacaagtg tattaggggac aacaactgca tttgcagaag aaaatgggaa gagcgcacag 120

ctcggtgattc acaaaaaagaa aatgacggat ttaccagatc cgcttattca aaatagcggg 180

aaagaaaatga gcgagtttga taaatatcaa ggactggcag atgtgacgtt tagtatttat 240

aacgtgacga acgaatttta cgagcaacga gcggcaggcg caagcgttga tgcagctaaa 300  
caagctgtcc aaagtttaac tcctggaaa cctgttgctc aaggaaccac cgatgcaaat 360  
ggaaatgtca ctgttcagtt acctaaaaaa caaatggta aagatgcagt gtataccatt 420  
aaagaagaac caaaagaggg tgtagttgct gctacgaata tgggggtggc gttcccaagtt 480  
tacgaaatga tcaagcaaac agatggttcc tataaatatg gaacagaaga attagcggtt 540  
gttcatattt atcctaaaaaa tgtggtagcc aatgatggta gtttacatgt gaaaaaaagta 600  
ggaactgctg aaaatgaagg attaaatggc gcagaatttg ttatttctaa aagcgaaggc 660  
tcaccaggca cagtaaaata tatccaagga gtcaaagatg gattatatac atggacaacg 720  
gataaagaac aagcaaaacg ctttattact gggaaaagtt atgaaattgg cgaaaatgat 780  
ttcacagaag cagagaatgg aacgggagaa ttaacagttt aaaaatcttga ggttggttcg 840  
tatattttag aagaagtaaa agctccaaat aatgcagaat taattgaaaa tcaaacaaaa 900  
acaccattta caattgaagc aaacaatcaa acacctgtt aaaaaacagt caaaaatgat 960  
acctctaaag ttgataaaac aacaccaagc ttagatggta aagatgtggc aattggcgaa 1020  
aaaattaaat atcaaatttc tgtaaatatt ccattggga ttgcagacaa agaaggcgac 1080  
gctaataaaat acgtcaaattt caatttagtt gataaacatg atgcagcctt aactttttagt 1140  
aacgtgactt ctggagagta tgcttatgct ttatatgtt gggatacagt gattgctcct 1200  
gaaaattatc aagtgactga acaagcaaattt ggcttcactg tcgcccgtt tccagcgtat 1260  
attcctacgc taacaccagg cggcacacta aaattcgttt actttatgca .tttaaatgaa 1320  
aaagcagatc ctacgaaagg cttaaaaat gaggcgaatg ttgataacgg tcataaccgac 1380  
gaccaaacac caccaactgt tgaagttgtt acaggtggga aacgtttcat taaagtgcgt 1440  
ggcgatgtga cagcgacaca agccttggcg ggagcttcct ttgtcgtccg tgcataaaac 1500  
agcgacacag caaatttattt gaaaatcgat gaaacaacga aagcagcaac ttgggtgaaa 1560  
acaatggctt aagcaactac ttttacaaca acggctgtat gattagttga tttcacaggg 1620  
cttaatacg gtaccttattt tttagaaagaa actgttagctc ctgtatgatta tttgttgcgtt 1680  
acaatcgaa ttgaattttgtt ggtcaatgaa caatcatatg gcacaacaga aaaccttagtt 1740  
tcaccagaaa aagtacccaaa caaacacaaa ggtaccttac cttcaacagg tggcaaagga 1800  
atctacgtttt acttaggaag tggcgtagtc ttgtacttta ttgcaggagt ctactttgtt 1860  
agacgttagaa aagaaaaatgc t 1881

<210> 13

<211> 627

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 13

Met Lys Gln Leu Lys Lys Val Trp Tyr Thr Val Ser Thr Leu Leu Leu  
1 5 10 15

Ile Leu Pro Leu Phe Thr Ser Val Leu Gly Thr Thr Ala Phe Ala  
20 25 30

Glu Glu Asn Gly Glu Ser Ala Gln Leu Val Ile His Lys Lys Lys Met  
35 40 45

Thr Asp Leu Pro Asp Pro Leu Ile Gln Asn Ser Gly Lys Glu Met Ser  
50 55 60

Glu Phe Asp Lys Tyr Gln Gly Leu Ala Asp Val Thr Phe Ser Ile Tyr  
65 70 75 80

Asn Val Thr Asn Glu Phe Tyr Glu Gln Arg Ala Ala Gly Ala Ser Val  
85 90 95

Asp Ala Ala Lys Gln Ala Val Gln Ser Leu Thr Pro Gly Lys Pro Val  
100 105 110

Ala Gln Gly Thr Thr Asp Ala Asn Gly Asn Val Thr Val Gln Leu Pro  
115 120 125

Lys Lys Gln Asn Gly Lys Asp Ala Val Tyr Thr Ile Lys Glu Glu Pro  
130 135 140

Lys Glu Gly Val Val Ala Ala Thr Asn Met Val Val Ala Phe Pro Val  
145 150 155 160

Tyr Glu Met Ile Lys Gln Thr Asp Gly Ser Tyr Lys Tyr Gly Thr Glu  
165 170 175

Glu Leu Ala Val Val His Ile Tyr Pro Lys Asn Val Val Ala Asn Asp  
180 185 190

Gly Ser Leu His Val Lys Lys Val Gly Thr Ala Glu Asn Glu Gly Leu

195

200

205

Asn Gly Ala Glu Phe Val Ile Ser Lys Ser Glu Gly Ser Pro Gly Thr  
210 215 220

Val Lys Tyr Ile Gln Gly Val Lys Asp Gly Leu Tyr Thr Trp Thr Thr  
225 230 235 240

Asp Lys Glu Gln Ala Lys Arg Phe Ile Thr Gly Lys Ser Tyr Glu Ile  
245 250 255

Gly Glu Asn Asp Phe Thr Glu Ala Glu Asn Gly Thr Gly Glu Leu Thr  
260 265 270

Val Lys Asn Leu Glu Val Gly Ser Tyr Ile Leu Glu Glu Val Lys Ala  
275 280 285

Pro Asn Asn Ala Glu Leu Ile Glu Asn Gln Thr Lys Thr Pro Phe Thr  
290 295 300

Ile Glu Ala Asn Asn Gln Thr Pro Val Glu Lys Thr Val Lys Asn Asp  
305 310 315 320

Thr Ser Lys Val Asp Lys Thr Thr Pro Ser Leu Asp Gly Lys Asp Val  
325 330 335

Ala Ile Gly Glu Lys Ile Lys Tyr Gln Ile Ser Val Asn Ile Pro Leu  
340 345 350

Gly Ile Ala Asp Lys Glu Gly Asp Ala Asn Lys Tyr Val Lys Phe Asn  
355 360 365

Leu Val Asp Lys His Asp Ala Ala Leu Thr Phe Asp Asn Val Thr Ser  
370 375 380

Gly Glu Tyr Ala Tyr Ala Leu Tyr Asp Gly Asp Thr Val Ile Ala Pro  
385 390 395 400

Glu Asn Tyr Gln Val Thr Glu Gln Ala Asn Gly Phe Thr Val Ala Val  
405 410 415

Asn Pro Ala Tyr Ile Pro Thr Leu Thr Pro Gly Gly Thr Leu Lys Phe  
420 425 430

Val Tyr Phe Met His Leu Asn Glu Lys Ala Asp Pro Thr Lys Gly Phe  
435 440 445

Lys Asn Glu Ala Asn Val Asp Asn Gly His Thr Asp Asp Gln Thr Pro  
450 455 460

Pro Thr Val Glu Val Val Thr Gly Gly Lys Arg Phe Ile Lys Val Asp  
465 470 475 480

Gly Asp Val Thr Ala Thr Gln Ala Leu Ala Gly Ala Ser Phe Val Val  
485 490 495

Arg Asp Gln Asn Ser Asp Thr Ala Asn Tyr Leu Lys Ile Asp Glu Thr  
500 505 510

Thr Lys Ala Ala Thr Trp Val Lys Thr Lys Ala Glu Ala Thr Thr Phe  
515 520 525

Thr Thr Thr Ala Asp Gly Leu Val Asp Ile Thr Gly Leu Lys Tyr Gly  
530 535 540

Thr Tyr Tyr Leu Glu Glu Thr Val Ala Pro Asp Asp Tyr Val Leu Leu  
545 550 555 560

Thr Asn Arg Ile Glu Phe Val Val Asn Glu Gln Ser Tyr Gly Thr Thr  
565 570 575

Glu Asn Leu Val Ser Pro Glu Lys Val Pro Asn Lys His Lys Gly Thr  
580 585 590

Leu Pro Ser Thr Gly Gly Lys Gly Ile Tyr Val Tyr Leu Gly Ser Gly  
595 600 605

Ala Val Leu Leu Leu Ile Ala Gly Val Tyr Phe Ala Arg Arg Arg Lys  
610 615 620

Glu Asn Ala  
625

<210> 14  
<211> 3387  
<212> DNA

<213> *Staphylococcus epidermidis*

<400> 14  
atgacgacca caggaaagaa actgaaagtt atttcatgc tgataatatt gagtttatca 60  
aactttgtgc cattatctgc aatagcagac actacagatg atccaacagt tttagaaaca 120  
atttcagctg aagtcatttc ggatcagtct ggaaaaaaag cactgaacat caagctaaat 180  
gcgaataaca ccagtgctga aaagatagaa aaagaaattg gtctagtcga aaattactta 240  
agtgatgtgg aaagaaaaga aggagatggc tatgcttatac aggtaaatag cggaaaatt 300  
acgttggaaa tctcatcaaa cactaaacaa actatcgatc tgagtttcc aatcgatcca 360  
gcactttacc acagccaggc aaacaagctg atcgtcgata ataaagaata tgacattatt 420  
gatgagacag aaaataagaa agatacagat gtgtcagtac caaagccaga cgaatagaa 480  
gaagaatcat caaaagaaaa cgaaaattct gtcagccat ttacattgcc tacattatcc 540  
ttgccagctg tgagtgtgcc atctaatac acgattccta cagaatatac aacagatgat 600  
cagggcactt atcctaaagc cagttggcaa cctacaggaa atacaaatgt tcttgatcat 660  
caaggcaata aaaacggaac aaatcaatgg gatggataa attcttggaa tggagatcct 720  
aatgatcgga cccattcgta tatcgaatat ggaggaaccg gtaatcaagc agactatgct 780  
atacgaaagt atgcaaagga aacaagtaca cccggattgt ttgatgtta tttgaatgct 840  
cgtggaaatg tacaaaaaga tatcacgcct cttgatctcg tattggctgt agactggta 900  
ggaagtatga acgacaataa tcggatcggt gaagtaaaga ttgggtcgta tcgaaaaatc 960  
gatacttag cagatagcgg tatcacagac aaaatcaata tgggatatgt cggctactca 1020  
agcgaaggat atagctacag taacggtgca gtacagatgg gttcatttga ttcaatgt 1080  
aatcaagtaa aatccattac accttcacgg acaaattggtg gtactttac acaaaaagca 1140  
ctaagagatg caggaagcat gctatccgtt ccaaattggac ataaaaaaatg gatcgaaaa 1200  
ctgacggatg gtgtaccaac atttcctat aaagtacagc gggtacacgc acaatcaagc 1260  
agcaattatt acggaactca gtttctaat acgcaagatc ggcggggaaa tacttctcta 1320  
atctcaagaa tctatgatgc acctgaccaa aacaatctat ccagaagaat cgacagtacg 1380  
tttatcgcaa ccatcgaga agcgatggca ctcaaagaac gaggaatcgaa aatacatgg 1440  
cttggcatcc aacttcaaag cgatccggca gctggctct caaaagcaga agtagagtct 1500  
cgtatgcgac aaatggtttc atcagatgaa aaaggcgatc tttactatga atcagctgat 1560  
catgcaacag atatctctga atacctagcc aaaaaagctg tacagatctc agcaactgt 1620

agcaatggac aaataaatga tccaatcgca gaaccattca tttatcagcc tggcacatt 1680  
tcagtcaaga gtgtggggac aagtcctaca acggtcactc catctatttc catagaagga 1740  
aataccatca agagcaatca gatctattta ggaaaagacc aagaaatcca aatccattac 1800  
caagtgagaa tccaaacaga aaatgaggac ttccatccaa atttctggta tcaaataaac 1860  
ggcaggacaa ctttccagcc aaacattgtt accaatgaat tagctgaatt cggtatacca 1920  
tctgctaaag ctcccggagt cagtcttcac atcaaaaagt tatggaaaga atttgacaac 1980  
aatctagctg atcgtccaga tcaagttact tttgagattc aacgggaaca tacgacaaat 2040  
gctgcagctt ggaaaaacgg atatattcga atcattaaac cagctaaaga tacaacaaat 2100  
acgtggaaac gtgcagacat tgacaaatta tctgcaaata gcggagaaag ttatcaagag 2160  
atattatcac tacctcaata caataatcaa ggtcaagcat tcaagttacca aacaatcaa 2220  
gaattacctg taccaggata cgattctcaa caaatagatg caatgacatg gaaaaatact 2280  
aaacaattca caccgttaaa ctgaaaata acgaaaaatt cctctacagg tgaaaaggat 2340  
cttattggcg ctgtttcaa attaacagga gattctattt atactttact aacagatcat 2400  
ggcgacggaa cctattctct tccagaaaat gtcaaattgc aaaaagaaat gacctatacg 2460  
ctgacagaaa caaaagctcc agaagggcat ggattaagca aaaagactac ttggaaatc 2520  
aagatcgctt ctgatggtac ggtaaccatt gatggaaaaa cagtcactac ttccgatgt 2580  
acgatccagt tgactattga aaatcctttt gttgaagttc ctgttagcagt acgtaagtat 2640  
gcgatgcaag ggacggacaa agagataaaat cttaaaggag cagcatttc cctacagaaa 2700  
aaagaagcaa atggtactta tcagccaatt gacagccaaa caacgaatga aaaaggtctt 2760  
gccagtttg attcactcac acctggtaaa tatcgactcg ttgaaacagc tggcctgccc 2820  
ggatatgata cttcgccggg aaattatgaa ttccaaatcg ataaatatgg aaaaatcatt 2880  
tacacggaa aaaataccga gatgacaaat aatgtatgga cgctcactca tcaaaatcga 2940  
ctaaaagcgt ttgatctaac ggtacacaaa aaagaagaca acggacagac attaaaagga 3000  
gcaaaattca gactgcaggg accagaaaatg gacttagaat cgccaaaaga tggacaagaa 3060  
acagataacct ttctattcga aaatttaaaa cctggaactt atacgctgac cgaaactttt 3120  
acaccagaag gataccaaagg tctaaaagag ccagttacta tagttataca cgaagatggg 3180  
tcaattcaag tggatggaca agatcatgaa tctgttctgt caccaggagc caaaaacaac 3240  
cagatttctt tagacatcac gaatcaggca aaagtaccat tacctgaaac gggaggaatt 3300  
ggccgttag gaatctatct agtagggatg attgggtgtg cgtttctat ttggatctt 3360

tttttgaaaa aagaaagagg gggcagc

3387

<210> 15

<211> 1129

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 15

Met Thr Thr Thr Gly Lys Lys Leu Lys Val Ile Phe Met Leu Ile Ile  
1 5 10 15

Leu Ser Leu Ser Asn Phe Val Pro Leu Ser Ala Ile Ala Asp Thr Thr  
20 25 30

Asp Asp Pro Thr Val Leu Glu Thr Ile Ser Ala Glu Val Ile Ser Asp  
35 40 45

Gln Ser Gly Lys Lys Ala Leu Asn Ile Lys Leu Asn Ala Asn Asn Thr  
50 55 60

Ser Ala Glu Lys Ile Glu Lys Glu Ile Gly Leu Val Glu Asn Tyr Leu  
65 70 75 80

Ser Asp Val Glu Arg Lys Glu Gly Asp Gly Tyr Ala Tyr Gln Val Asn  
85 90 95

Ser Gly Lys Ile Thr Leu Glu Ile Ser Ser Asn Thr Lys Gln Thr Ile  
100 105 110

Asp Leu Ser Phe Pro Ile Asp Pro Ala Leu Tyr His Ser Gln Ala Asn  
115 120 125

Lys Leu Ile Val Asp Asn Lys Glu Tyr Asp Ile Ile Asp Glu Thr Glu  
130 135 140

Asn Lys Lys Asp Thr Asp Val Ser Val Pro Lys Pro Asp Glu Ile Glu  
145 150 155 160

Glu Glu Ser Ser Lys Glu Asn Glu Asn Ser Val Ser Pro Phe Thr Leu  
165 170 175

Pro Thr Leu Ser Leu Pro Ala Val Ser Val Pro Ser Asn Gln Thr Ile  
180 185 190

Pro Thr Glu Tyr Thr Thr Asp Asp Gln Gly Thr Tyr Pro Lys Ala Ser  
195 200 205

Trp Gln Pro Thr Gly Asn Thr Asn Val Leu Asp His Gln Gly Asn Lys  
210 215 220

Asn Gly Thr Asn Gln Trp Asp Gly Ile Asn Ser Trp Asn Gly Asp Pro  
225 230 235 240

Asn Asp Arg Thr His Ser Tyr Ile Glu Tyr Gly Gly Thr Gly Asn Gln  
245 250 255

Ala Asp Tyr Ala Ile Arg Lys Tyr Ala Lys Glu Thr Ser Thr Pro Gly  
260 265 270

Leu Phe Asp Val Tyr Leu Asn Ala Arg Gly Asn Val Gln Lys Asp Ile  
275 280 285

Thr Pro Leu Asp Leu Val Leu Val Val Asp Trp Ser Gly Ser Met Asn  
290 295 300

Asp Asn Asn Arg Ile Gly Glu Val Lys Ile Gly Val Asp Arg Phe Val  
305 310 315 320

Asp Thr Leu Ala Asp Ser Gly Ile Thr Asp Lys Ile Asn Met Gly Tyr  
325 330 335

Val Gly Tyr Ser Ser Glu Gly Tyr Ser Tyr Ser Asn Gly Ala Val Gln  
340 345 350

Met Gly Ser Phe Asp Ser Val Lys Asn Gln Val Lys Ser Ile Thr Pro  
355 360 365

Ser Arg Thr Asn Gly Gly Thr Phe Thr Gln Lys Ala Leu Arg Asp Ala  
370 375 380

Gly Ser Met Leu Ser Val Pro Asn Gly His Lys Lys Val Ile Val Leu  
385 390 395 400

Leu Thr Asp Gly Val Pro Thr Phe Ser Tyr Lys Val Gln Arg Val His  
405 410 415

Ala Gln Ser Ser Ser Asn Tyr Tyr Gly Thr Gln Phe Ser Asn Thr Gln  
420 425 430

Asp Arg Pro Gly Asn Thr Ser Leu Ile Ser Arg Ile Tyr Asp Ala Pro  
435 440 445

Asp Gln Asn Asn Leu Ser Arg Arg Ile Asp Ser Thr Phe Ile Ala Thr  
450 455 460

Ile Gly Glu Ala Met Ala Leu Lys Glu Arg Gly Ile Glu Ile His Gly  
465 470 475 480

Leu Gly Ile Gln Leu Gln Ser Asp Pro Ala Ala Gly Leu Ser Lys Ala  
485 490 495

Glu Val Glu Ser Arg Met Arg Gln Met Val Ser Ser Asp Glu Lys Gly  
500 505 510

Asp Leu Tyr Tyr Glu Ser Ala Asp His Ala Thr Asp Ile Ser Glu Tyr  
515 520 525

Leu Ala Lys Lys Ala Val Gln Ile Ser Ala Thr Val Ser Asn Gly Gln  
530 535 540

Ile Asn Asp Pro Ile Ala Glu Pro Phe Ile Tyr Gln Pro Gly Thr Leu  
545 550 555 560

Ser Val Lys Ser Val Gly Thr Ser Pro Thr Thr Val Thr Pro Ser Ile  
565 570 575

Ser Ile Glu Gly Asn Thr Ile Lys Ser Asn Gln Ile Tyr Leu Gly Lys  
580 585 590

Asp Gln Glu Ile Gln Ile His Tyr Gln Val Arg Ile Gln Thr Glu Asn  
595 600 605

Glu Asp Phe His Pro Asn Phe Trp Tyr Gln Met Asn Gly Arg Thr Thr  
610 615 620

Phe Gln Pro Asn Ile Asp Thr Asn Glu Leu Ala Glu Phe Gly Ile Pro  
625 630 635 640

Ser Ala Lys Ala Pro Gly Val Ser Leu His Ile Lys Lys Leu Trp Glu  
645 650 655

Glu Phe Asp Asn Asn Leu Ala Asp Arg Pro Asp Gln Val Thr Phe Glu  
660 665 670

Ile Gln Arg Glu His Thr Thr Asn Ala Ala Ala Trp Lys Asn Gly Tyr  
675 680 685

Ile Arg Ile Ile Lys Pro Ala Lys Asp Thr Thr Asn Thr Trp Glu Arg  
690 695 700

Ala Asp Ile Asp Lys Leu Ser Ala Asn Ser Gly Glu Ser Tyr Gln Glu  
705 710 715 720

Ile Leu Ser Leu Pro Gln Tyr Asn Asn Gln Gly Gln Ala Phe Ser Tyr  
725 730 735

Gln Thr Ile Lys Glu Leu Pro Val Pro Gly Tyr Asp Ser Gln Gln Ile  
740 745 750

Asp Ala Met Thr Trp Lys Asn Thr Lys Gln Phe Thr Pro Leu Asn Leu  
755 760 765

Lys Ile Thr Lys Asn Ser Ser Thr Gly Glu Lys Asp Leu Ile Gly Ala  
770 775 780

Val Phe Lys Leu Thr Gly Asp Ser Ile Asp Thr Leu Leu Thr Asp His  
785 790 795 800

Gly Asp Gly Thr Tyr Ser Leu Pro Glu Asn Val Lys Leu Gln Lys Glu  
805 810 815

Met Thr Tyr Thr Leu Thr Glu Thr Lys Ala Pro Glu Gly His Gly Leu  
820 825 830

Ser Lys Lys Thr Thr Trp Glu Ile Lys Ile Ala Ser Asp Gly Thr Val  
835 840 845

Thr Ile Asp Gly Lys Thr Val Thr Thr Ser Asp Asp Thr Ile Gln Leu  
850 855 860

Thr Ile Glu Asn Pro Phe Val Glu Val Pro Val Ala Val Arg Lys Tyr

865                    870                    875                    880  
Ala Met Gln Gly Thr Asp Lys Glu Ile Asn Leu Lys Gly Ala Ala Phe  
                  885                    890                    895  
  
Ser Leu Gln Lys Lys Glu Ala Asn Gly Thr Tyr Gln Pro Ile Asp Ser  
                  900                    905                    910  
  
Gln Thr Thr Asn Glu Lys Gly Leu Ala Ser Phe Asp Ser Leu Thr Pro  
                  915                    920                    925  
  
Gly Lys Tyr Arg Val Val Glu Thr Ala Gly Pro Ala Gly Tyr Asp Thr  
                  930                    935                    940  
  
Ser Pro Gly Asn Tyr Glu Phe Gln Ile Asp Lys Tyr Gly Lys Ile Ile  
                  945                    950                    955                    960  
  
Tyr Thr Gly Lys Asn Thr Glu Met Thr Asn Asn Val Trp Thr Leu Thr  
                  965                    970                    975  
  
His Gln Asn Arg Leu Lys Ala Phe Asp Leu Thr Val His Lys Lys Glu  
                  980                    985                    990  
  
Asp Asn Gly Gln Thr Leu Lys Gly Ala Lys Phe Arg Leu Gln Gly Pro  
                  995                    1000                    1005  
  
Glu Met Asp Leu Glu Ser Pro Lys Asp Gly Gln Glu Thr Asp Thr  
                  1010                    1015                    1020  
  
Phe Leu Phe Glu Asn Leu Lys Pro Gly Thr Tyr Thr Leu Thr Glu  
                  1025                    1030                    1035  
  
Thr Phe Thr Pro Glu Gly Tyr Gln Gly Leu Lys Glu Pro Val Thr  
                  1040                    1045                    1050  
  
Ile Val Ile His Glu Asp Gly Ser Ile Gln Val Asp Gly Gln Asp  
                  1055                    1060                    1065  
  
His Glu Ser Val Leu Ser Pro Gly Ala Lys Asn Asn Gln Ile Ser  
                  1070                    1075                    1080  
  
Leu Asp Ile Thr Asn Gln Ala Lys Val Pro Leu Pro Glu Thr Gly  
                  1085                    1090                    1095

Gly Ile Gly Arg Leu Gly Ile Tyr Leu Val Gly Met Ile Gly Cys  
1100 1105 1110

Ala Phe Ser Ile Trp Tyr Leu Phe Leu Lys Lys Glu Arg Gly Gly  
1115 1120 1125

Ser

<210> 16  
<211> 1422  
<212> DNA  
<213> *Staphylococcus epidermidis*

<400> 16	
atgaaaaaac ttgggtggct tagtatgtgt ctcttcttgt tactatttaa accagcttt	60
actcaggtag caacagaaac agaaacagaa atggttcaga ttactttaca caaattgctt	120
ttcccaaacg ggcaactgcc gaaaaatcat ccaaattgacg gacaagaaaa agctttatta	180
caaacgtatc gaggattaaa tgggtgtcaca ttccaagttt atgatgtcac agattcttt	240
taccatctac gggaaaaggg caaaacggta gaagaagcac aagcagagat cgcaaaaaac	300
ggtgcgtctt ccggatgttt tacccgagaa gcaacaacta caactcttaa caacgaagat	360
ggtatcgctt cttttctct ggccgctaaa gatcaagaaa aaagagataa agcgtatctt	420
ttcattgaat ccaaagtacc agaagtcgtc aaagaaaagg cagagaatat ggtatgttt	480
cttcctgtac atggacaaaa caatcaaaaa ctttcaacta tccatttgc tcctaaaaat	540
gaagaaaaacg actaccctga tccacccccc gagaaggat tagaagagcc tagaaatgat	600
tttacgattt gtgaaaaat cacttattcc ttgcatacga caattcctgt aaatatcctt	660
gactatcaaa agttcgattt gtcagatgt gcggatgtaa cattaacgtt tttacctaatt	720
agtttaacga tttcatcgaa tggagaaaaag ctgacagaag gctttgtcat acacaagaaa	780
cctcacggat ttgatgtttt atttcgatc cttcggtgg aaaaatatgc tggaaaaaaa	840
ctgaccattt cttatcagat gcagactaagc agtacagcac aggcgaacaa ggaaatcaac	900
aacaacggaa cactggattt tgggtttgggt gtcagttacaa agaaagtctc tgtatataca	960
gggagtaagc aatttgcattt aatcgagaca aataaaccag ataaacgatt agctggcgca	1020
gtattcctta ttaaaaacaa agcaggaaat tacctccagc aaacagccaa cggatacaag	1080
tggacaaaga acgaatcaga tgcgcgttcac ctgattccg ataaaaatgg cgcttttca	1140

atttccgggt	tgaaaacagg	aagttatcga	ttaaaagaga	tcgaagcacc	ttctggttat	1200
attttaagtg	aaacagaaat	tccgtttacc	atttcaactt	ttctttctga	ggataaagag	1260
gcggacagta	tattgaaagt	agtcaataaa	aaagaaaata	gccgtccatt	tcttccaaaa	1320
acaaacgaaa	cgaaaaatac	acttttaggc	gttgttgta	tggtattcgc	aagcttgca	1380
atctggtgt	ttatcaaaaa	aagaacagga	gtgaaaaat	ga		1422

<210> 17  
<211> 473  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 17

Met	Lys	Lys	Leu	Gly	Trp	Leu	Ser	Met	Cys	Leu	Phe	Leu	Leu	Phe
1								10					15	

Lys	Pro	Ala	Phe	Thr	Gln	Val	Ala	Thr	Glu	Thr	Glu	Thr	Glu	Met	Val
								25					30		

Gln	Ile	Thr	Leu	His	Lys	Leu	Leu	Phe	Pro	Asn	Gly	Gln	Leu	Pro	Lys
								40				45			

Asn	His	Pro	Asn	Asp	Gly	Gln	Glu	Lys	Ala	Leu	Leu	Gln	Thr	Tyr	Arg
							55				60				

Gly	Leu	Asn	Gly	Val	Thr	Phe	Gln	Val	Tyr	Asp	Val	Thr	Asp	Ser	Phe
							65		70		75		80		

Tyr	His	Leu	Arg	Glu	Lys	Gly	Lys	Thr	Val	Glu	Glu	Ala	Gln	Ala	Glu
								85		90		95			

Ile	Ala	Lys	Asn	Gly	Ala	Ser	Ser	Gly	Met	Phe	Thr	Ala	Glu	Ala	Thr
								100		105		110			

Thr	Thr	Thr	Leu	Asn	Asn	Glu	Asp	Gly	Ile	Ala	Ser	Phe	Ser	Leu	Ala
								115		120		125			

Ala	Lys	Asp	Gln	Glu	Lys	Arg	Asp	Lys	Ala	Tyr	Leu	Phe	Ile	Glu	Ser
								130		135		140			

Lys	Val	Pro	Glu	Val	Val	Lys	Glu	Lys	Ala	Glu	Asn	Met	Val	Val	Val
								145		150		155		160	

Leu Pro Val His Gly Gln Asn Asn Gln Lys Leu Ser Thr Ile His Leu  
165 170 175

Tyr Pro Lys Asn Glu Glu Asn Asp Tyr Pro Asp Pro Pro Phe Glu Lys  
180 185 190

Val Leu Glu Glu Pro Arg Asn Asp Phe Thr Ile Gly Glu Lys Ile Thr  
195 200 205

Tyr Ser Leu His Thr Thr Ile Pro Val Asn Ile Leu Asp Tyr Gln Lys  
210 215 220

Phe Glu Leu Ser Asp Ser Ala Asp Glu Ala Leu Thr Phe Leu Pro Asn  
225 230 235 240

Ser Leu Thr Ile Ser Ser Asn Gly Glu Lys Leu Thr Glu Gly Phe Val  
245 250 255

Ile His Lys Lys Pro His Gly Phe Asp Val Leu Phe Ser Ile Pro Ser  
260 265 270

Leu Glu Lys Tyr Ala Gly Lys Lys Leu Thr Ile Ser Tyr Gln Met Gln  
275 280 285

Leu Ser Ser Thr Ala Gln Ala Asn Lys Glu Ile Asn Asn Asn Gly Thr  
290 295 300

Leu Asp Phe Gly Phe Gly Val Ser Thr Lys Lys Val Ser Val Tyr Thr  
305 310 315 320

Gly Ser Lys Gln Phe Val Lys Ile Glu Thr Asn Lys Pro Asp Lys Arg  
325 330 335

Leu Ala Gly Ala Val Phe Leu Ile Lys Asn Lys Ala Gly Asn Tyr Leu  
340 345 350

Gln Gln Thr Ala Asn Gly Tyr Lys Trp Thr Lys Asn Glu Ser Asp Ala  
355 360 365

Leu His Leu Ile Ser Asp Lys Asn Gly Ala Phe Ser Ile Ser Gly Leu  
370 375 380

Lys Thr Gly Ser Tyr Arg Leu Lys Glu Ile Glu Ala Pro Ser Gly Tyr  
385 390 395 400

Ile Leu Ser Glu Thr Glu Ile Pro Phe Thr Ile Ser Thr Phe Leu Ser  
405 410 415

Glu Asp Lys Glu Ala Asp Ser Ile Leu Lys Val Val Asn Lys Lys Glu  
420 425 430

Asn Ser Arg Pro Phe Leu Pro Lys Thr Asn Glu Thr Lys Asn Thr Leu  
435 440 445

Leu Gly Val Val Gly Met Val Phe Ala Ser Phe Ala Ile Trp Leu Phe  
450 455 460

Ile Lys Lys Arg Thr Gly Val Lys Lys  
465 470

<210> 18  
<211> 1878  
<212> DNA  
<213> *Staphylococcus epidermidis*

<400> 18  
atgaaaaatc ataaaaaaat aaacgttatg ttaggagtcc tttccttat tttaccatta 60  
ctcacaaaca gcttcggcgc aaaaaaaagtq tttgcagagg agacagcagc tcaagtcatc 120  
cttcataaaa agaaaatgac tgatttaccc gatcctttaa tccaaaacag cggaaagaa 180  
atgagcgaat tcgatcaata ccaaggatta gccgatattt cattttcagt ttataacgtc 240  
actcaagaat tttatgcgca acgagataaa ggagcgtccg tggatgcagc aaaacaagca 300  
gtccagtc ttgactcctgg tacaccagtt gcttcaggaa cgacagatgc tggatggaaat 360  
gtcactttat cttaacctaa aaaacaaaat gggaaagatg cagtctacac gatcaaagaa 420  
gaaccaaaaag acggagtgtc agctgccgca aacatggtt tagcttccc tgtatatgag 480  
atgatcaaac aagcagatgg ctcttataaa tacggacag aagaactaga tactatccat 540  
ctctacccta aaaatacagt cggtaatgat ggaacgttga aagttacaaa aatcggtact 600  
gccgaaaaacg aagcactaaa tggagcagaa tttattttt ctaaagaaga aggaacacca 660  
agcgtcaaaa aatacatcca aagtgtcaca gatggattgt acacttggac aactgatcaa 720  
accaaagcca aacatttcat tactggtcat tcttatgaca tcggcaacaa tgactttgcc 780

Lys Thr Gly Ser Tyr Arg Leu Lys Glu Ile Glu Ala Pro Ser Gly Tyr  
385 390 395 400

Ile Leu Ser Glu Thr Glu Ile Pro Phe Thr Ile Ser Thr Phe Leu Ser  
405 410 415

Glu Asp Lys Glu Ala Asp Ser Ile Leu Lys Val Val Asn Lys Lys Glu  
420 425 430

Asn Ser Arg Pro Phe Leu Pro Lys Thr Asn Glu Thr Lys Asn Thr Leu  
435 440 445

Leu Gly Val Val Gly Met Val Phe Ala Ser Phe Ala Ile Trp Leu Phe  
450 455 460

Ile Lys Lys Arg Thr Gly Val Lys Lys  
465 470

<210> 18  
<211> 1878  
<212> DNA  
<213> *Staphylococcus epidermidis*

<400> 18  
atgaaaaatc ataaaaaaat aaacgtttagt ttaggagtcc ttttccttat tttaccatta 60  
ctcacaaaaca gttcggcgc aaaaaaaagtg tttgcagagg agacagcagc tcaagtcatc  
cttcataaaa agaaaatgac tgatttaccc gatcctttaa tccaaaacag cggaaagaa 120  
atgagcgaat tcgatcaata ccaaggatta gccgatattt cattttcagt ttataacgtc  
actcaagaat tttatgcgca acgagataaa ggagcgtccg tggatgcagc aaaacaagca 180  
gtccagtctt tgactcctgg tacaccagtt gttcaggaa cgacagatgc tggatggaaat  
gtcactttat cttaacctaa aaaacaaaat gggaaagatg cagtctacac gatcaaagaa 240  
gaaccaaaaag acggagtgtc agctgccgca aacatggtt tagcttccc tgtatatgag  
atgatcaaac aagcagatgg ctcttataaa tacggacag aagaactaga tactatccat  
ctctacccta aaaatacagt cggtaatgat ggaacgttga aagttacaaa aatcggtact 300  
gccgaaaaacg aagcactaaa tggagcagaa tttatttattt ctaaagaaga aggaacacca  
agcgtcaaaa aatacatcca aagtgtcaca gatggattgt acacttggac aactgatcaa 360  
acccaaagcca aacatttcat tactggtcat tcttatgaca tcggcaacaa tgactttgcc 420  
480  
540  
600  
660  
720  
780

gaggcatcta ttgaaaaagg ccagttgatc gttaatcatt tagaagttgg aaaatataat	840
ttagaagaag taaaagctcc tgataatgcg gaaatgattg aaaagcaaac aatcacgcct	900
tttgagatcc tggcaaatacg ccaaacacca gtagaaaaga ccatcaaaaa tgatacgtct	960
aaagttgata aaacaacacc tcaattgaat ggaaaagatg tcgcaatcg tgaaaaatt	1020
caatatgaga tttctgtcaa tatccattt ggtatcgctg ataaagaagg aacgcaaaac	1080
aagtacacaa cattcaaact tatcgatact catgacgctg ctttaacatt tgataatgat	1140
tcttcagaa cgtatgctt tgcccttat gatggaaata aagaaatcga cccagtaaat	1200
tattctgtca ctgagcaaac agacggattc acggttcag ttgatccgaa ttatattcct	1260
tcatttaactc ctggcgtac attgaaattc gtttactata tgcatttcaa cgaaaaagca	1320
gatccaaacca aaggattttc taaccaagca aatgtcgata acgggcatac aaatgatcaa	1380
acaccaccgt cagtcgatgt cgttactggg ggcaaacgat ttgttaaagt agatggtgac	1440
gttacatcag accaaacact tgctggagca gaattcgtcg ttcgtgatca agatagtgac	1500
acagcgaaat atttatcgat cgacccatcc acaaaagccg tcagctgggt atcggcgaaa	1560
gaatcagcaa cggttttac aaccacaagt aacggttaa tcgatgtgac aggtctaaaa	1620
tatggcacgt actatctgga agaaacgaaa ggcgcagaaa aatatgttcc attaacaac	1680
cgtgttagcat ttactatcga tgaacaatct tatgtaacag caggacagtt gatttctcct	1740
gaaaaaaatac caaataaaaca caaaggtaaa cttccttcaa caggcgtaa ggaaatctat	1800
gtgtatatcg gtgcaggagt agtccttcta ctgattgctg gactgtactt tgctagacgc	1860
aagcacagtc agatttag	1878

<210> 19  
 <211> 625  
 <212> PRT  
 <213> *Staphylococcus epidermidis*  
 <400> 19

Met Lys Asn His Lys Lys Ile Asn Val Met Leu Gly Val Leu Phe Leu  
 1 5 10 15

Ile Leu Pro Leu Leu Thr Asn Ser Phe Gly Ala Lys Lys Val Phe Ala  
 20 25 30

Glu Glu Thr Ala Ala Gln Val Ile Leu His Lys Lys Lys Met Thr Asp  
 35 40 45

Leu Pro Asp Pro Leu Ile Gln Asn Ser Gly Lys Glu Met Ser Glu Phe  
50 55 60

Asp Gln Tyr Gln Gly Leu Ala Asp Ile Ser Phe Ser Val Tyr Asn Val  
65 70 75 80

Thr Gln Glu Phe Tyr Ala Gln Arg Asp Lys Gly Ala Ser Val Asp Ala  
85 90 95

Ala Lys Gln Ala Val Gln Ser Leu Thr Pro Gly Thr Pro Val Ala Ser  
100 105 110

Gly Thr Thr Asp Ala Asp Gly Asn Val Thr Leu Ser Leu Pro Lys Lys  
115 120 125

Gln Asn Gly Lys Asp Ala Val Tyr Thr Ile Lys Glu Glu Pro Lys Asp  
130 135 140

Gly Val Ser Ala Ala Asn Met Val Leu Ala Phe Pro Val Tyr Glu  
145 150 155 160

Met Ile Lys Gln Ala Asp Gly Ser Tyr Lys Tyr Gly Thr Glu Glu Leu  
165 170 175

Asp Thr Ile His Leu Tyr Pro Lys Asn Thr Val Gly Asn Asp Gly Thr  
180 185 190

Leu Lys Val Thr Lys Ile Gly Thr Ala Glu Asn Glu Ala Leu Asn Gly  
195 200 205

Ala Glu Phe Ile Ile Ser Lys Glu Glu Gly Thr Pro Ser Val Lys Lys  
210 215 220

Tyr Ile Gln Ser Val Thr Asp Gly Leu Tyr Thr Trp Thr Thr Asp Gln  
225 230 235 240

Thr Lys Ala Lys His Phe Ile Thr Gly His Ser Tyr Asp Ile Gly Asn  
245 250 255

Asn Asp Phe Ala Glu Ala Ser Ile Glu Lys Gly Gln Leu Ile Val Asn  
260 265 270

His Leu Glu Val Gly Lys Tyr Asn Leu Glu Glu Val Lys Ala Pro Asp  
275 280 285

Asn Ala Glu Met Ile Glu Lys Gln Thr Ile Thr Pro Phe Glu Ile Leu  
290 295 300

Ala Asn Ser Gln Thr Pro Val Glu Lys Thr Ile Lys Asn Asp Thr Ser  
305 310 315 320

Lys Val Asp Lys Thr Thr Pro Gln Leu Asn Gly Lys Asp Val Ala Ile  
325 330 335

Gly Glu Lys Ile Gln Tyr Glu Ile Ser Val Asn Ile Pro Leu Gly Ile  
340 345 350

Ala Asp Lys Glu Gly Thr Gln Asn Lys Tyr Thr Thr Phe Lys Leu Ile  
355 360 365

Asp Thr His Asp Ala Ala Leu Thr Phe Asp Asn Asp Ser Ser Gly Thr  
370 375 380

Tyr Ala Tyr Ala Leu Tyr Asp Gly Asn Lys Glu Ile Asp Pro Val Asn  
385 390 395 400

Tyr Ser Val Thr Glu Gln Thr Asp Gly Phe Thr Val Ser Val Asp Pro  
405 410 415

Asn Tyr Ile Pro Ser Leu Thr Pro Gly Gly Thr Leu Lys Phe Val Tyr  
420 425 430

Tyr Met His Leu Asn Glu Lys Ala Asp Pro Thr Lys Gly Phe Ser Asn  
435 440 445

Gln Ala Asn Val Asp Asn Gly His Thr Asn Asp Gln Thr Pro Pro Ser  
450 455 460

Val Asp Val Val Thr Gly Gly Lys Arg Phe Val Lys Val Asp Gly Asp  
465 470 475 480

Val Thr Ser Asp Gln Thr Leu Ala Gly Ala Glu Phe Val Val Arg Asp  
485 490 495

Gln Asp Ser Asp Thr Ala Lys Tyr Leu Ser Ile Asp Pro Ser Thr Lys

500

505

510

Ala Val Ser Trp Val Ser Ala Lys Glu Ser Ala Thr Val Phe Thr Thr  
515 520 525

Thr Ser Asn Gly Leu Ile Asp Val Thr Gly Leu Lys Tyr Gly Thr Tyr  
530 535 540

Tyr Leu Glu Glu Thr Lys Ala Pro Glu Lys Tyr Val Pro Leu Thr Asn  
545 550 555 560

Arg Val Ala Phe Thr Ile Asp Glu Gln Ser Tyr Val Thr Ala Gly Gln  
565 570 575

Leu Ile Ser Pro Glu Lys Ile Pro Asn Lys His Lys Gly Thr Leu Pro  
580 585 590

Ser Thr Gly Gly Lys Gly Ile Tyr Val Tyr Ile Gly Ala Gly Val Val  
595 600 605

Leu Leu Leu Ile Ala Gly Leu Tyr Phe Ala Arg Arg Lys His Ser Gln  
610 615 620

Ile  
625

<210> 20  
<211> 2402  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 20

Met Lys Asn Lys Gln Gly Phe Leu Pro Asn Leu Leu Asn Lys Tyr Gly  
1 5 10 15

Ile Arg Lys Leu Ser Ala Gly Thr Ala Ser Leu Leu Ile Gly Ala Thr  
20 25 30

Leu Val Phe Gly Ile Asn Gly Gln Val Lys Ala Ala Glu Thr Asp Asn  
35 40 45

Ile Val Ser Gln Asn Gly Asp Asn Lys Thr Asn Asp Ser Glu Ser Ser  
50 55 60

Asp Lys Glu Leu Val Lys Ser Glu Asp Asp Lys Thr Ser Ser Thr Ser  
65 70 75 80

Thr Asp Thr Asn Leu Glu Ser Glu Phe Asp Gln Asn Asn Asn Pro Ser  
85 90 95

Ser Ile Glu Glu Ser Thr Asn Arg Asn Asp Glu Asp Thr Leu Asn Gln  
100 105 110

Arg Thr Ser Thr Glu Thr Glu Lys Asp Thr His Val Lys Ser Ala Asp  
115 120 125

Thr Gln Thr Thr Asn Glu Thr Thr Asn Lys Asn Asp Asp Asn Ala Thr  
130 135 140

Thr Asn His Thr Glu Ser Ile Ser Asp Glu Ser Thr Tyr Gln Ser Asp  
145 150 155 160

Asp Ser Lys Thr Thr Gln His Asp Asn Ser Asn Thr Asn Gln Asp Thr  
165 170 175

Gln Ser Thr Leu Asn Pro Thr Ser Lys Glu Ser Ser Asn Lys Asp Glu  
180 185 190

Ala Thr Ser Pro Thr Pro Lys Glu Ser Thr Ser Ile Glu Lys Thr Asn  
195 200 205

Leu Ser Asn Asp Ala Asn His Gln Thr Thr Asp Glu Val Asn His Ser  
210 215 220

Asp Ser Asp Asn Met Thr Asn Ser Thr Pro Asn Asp Thr Glu Asn Glu  
225 230 235 240

Leu Asp Thr Thr Gln Leu Thr Ser His Asp Glu Ser Pro Ser Pro Gln  
245 250 255

Ser Asp Asn Phe Thr Gly Phe Thr Asn Leu Met Ala Thr Pro Leu Asn  
260 265 270

Leu Arg Asn Asp Asn Pro Arg Ile Asn Leu Leu Ala Ala Thr Glu Asp  
275 280 285

Thr Lys Pro Lys Thr Tyr Lys Lys Pro Asn Asn Ser Glu Tyr Ser Tyr  
290 295 300

Leu Leu Asn Asp Leu Gly Tyr Asp Ala Thr Thr Val Lys Glu Asn Ser  
305 310 315 320

Asp Leu Arg His Ala Gly Ile Ser Gln Ser Gln Asp Asn Thr Gly Ser  
325 330 335

Val Ile Lys Leu Asn Leu Thr Lys Trp Leu Ser Leu Gln Ser Asp Phe  
340 345 350

Val Asn Gly Gly Lys Val Asn Leu Ser Phe Ala Gln Ser Asp Phe Tyr  
355 360 365

Thr Gln Ile Glu Ser Ile Thr Leu Asn Asp Val Lys Met Asp Thr Thr  
370 375 380

Asn Asn Gly Gln Asn Trp Ser Ala Pro Ile Asn Gly Ser Thr Val Arg  
385 390 395 400

Ser Gly Leu Ile Gly Ser Val Thr Asn His Asp Ile Val Ile Thr Leu  
405 410 415

Lys Asn Ser Gln Thr Leu Ser Ser Leu Gly Tyr Ser Asn Asn Lys Pro  
420 425 430

Val Tyr Leu Thr His Thr Trp Thr Thr Asn Asp Gly Ala Ile Ala Glu  
435 440 445

Glu Ser Ile Gln Val Ala Ser Ile Thr Pro Thr Leu Asp Ser Lys Ala  
450 455 460

Pro Asn Thr Ile Gln Lys Ser Asp Phe Thr Ala Gly Arg Met Thr Asn  
465 470 475 480

Lys Ile Lys Tyr Asp Ser Ser Gln Asn Ser Ile Lys Ser Val His Thr  
485 490 495

Phe Lys Pro Asn Glu Asn Phe Leu Gln Thr Asp Tyr Arg Ala Val Leu  
500 505 510

Tyr Ile Lys Glu Gln Val Asn Lys Glu Leu Ile Pro Tyr Ile Asp Pro

515

520

525

Asn Ser Val Lys Leu Tyr Val Ser Asp Pro Asp Gly Asn Pro Ile Ser  
530 535 540

Gln Asp Arg Tyr Val Asn Gly Ser Ile Asp Asn Asp Gly Leu Phe Asp  
545 550 555 560

Ser Ser Lys Ile Asn Glu Ile Ser Ile Lys Asn Asn Asn Thr Ser Gly  
565 570 575

Gln Leu Ser Asn Ala Arg Thr Ser Leu Asp Arg Asn Val Phe Phe Gly  
580 585 590

Thr Leu Gly Gln Ser Arg Ser Tyr Thr Ile Ser Tyr Lys Leu Lys Asp  
595 600 605

Gly Tyr Thr Leu Glu Ser Val Ala Ser Lys Val Ser Ala Arg Glu Thr  
610 615 620

Phe Asp Ser Trp Met Glu Val Asp Tyr Leu Asp Ser Tyr Asp Ser Gly  
625 630 635 640

Ala Pro Asn Lys Arg Leu Leu Gly Ser Tyr Ala Ser Ser Tyr Ile Asp  
645 650 655

Met Ile Asp Arg Ile Pro Pro Val Ala Pro Lys Ala Asn Ser Ile Thr  
660 665 670

Thr Glu Asp Thr Ser Ile Lys Gly Thr Ala Glu Val Asp Thr Asn Ile  
675 680 685

Asn Leu Thr Phe Asn Asp Gly Arg Thr Leu Asn Gly Lys Val Asp Ser  
690 695 700

Asn Gly Asn Phe Ser Ile Ala Ile Pro Ser Tyr Tyr Val Leu Thr Gly  
705 710 715 720

Lys Glu Thr Ile Lys Ile Thr Ser Ile Asp Lys Gly Asp Asn Val Ser  
725 730 735

Pro Ala Ile Thr Ile Ser Val Ile Asp Lys Thr Pro Pro Ala Val Lys  
740 745 750

Ala Ile Ser Asn Lys Thr Gln Lys Val Asn Thr Glu Ile Glu Pro Ile  
755 760 765

Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val  
770 775 780

Glu Gly Leu Pro Ala Gly Met Thr Phe Asp Glu Ala Thr Asn Thr Ile  
785 790 795 800

Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr  
805 810 815

Thr Asp Glu Asn Gly Asn Ser Glu Thr Thr Thr Phe Thr Ile Asp Val  
820 825 830

Glu Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp Gln Thr Gln  
835 840 845

Glu Val Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr Asp Asn  
850 855 860

Ser Gly Arg Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asp Gly Val  
865 870 875 880

Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val  
885 890 895

Gly Ser Tyr Asp Ile Thr Val Thr Thr Asp Glu Ser Gly Asn Val  
900 905 910

Thr Glu Thr Ile Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro Thr  
915 920 925

Val Glu Ser Ile Ala Gly Gln Thr Gln Glu Val Asn Thr Glu Ile Glu  
930 935 940

Pro Ile Lys Ile Glu Ala Lys Asp Asn Ser Gly Gln Thr Val Thr Asn  
945 950 955 960

Lys Val Asp Gly Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr Asn  
965 970 975

Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Val Thr Val  
980 985 990

Thr Thr Thr Asp Glu Ser Gly Asn Ser Glu Thr Thr Thr Phe Thr Ile  
995 1000 1005

Glu Val Lys Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp  
1010 1015 1020

Gln Thr Gln Glu Val Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu  
1025 1030 1035

Ala Arg Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val Asp Gly  
1040 1045 1050

Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser  
1055 1060 1065

Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr  
1070 1075 1080

Thr Asp Glu Ser Gly Asn Val Thr Glu Thr Thr Phe Thr Ile Glu  
1085 1090 1095

Val Glu Asp Thr Thr Lys Pro Thr Val Glu Asn Val Ala Asp Gln  
1100 1105 1110

Thr Gln Glu Val Asn Thr Glu Ile Thr Pro Ile Thr Ile Glu Ser  
1115 1120 1125

Glu Asp Asn Ser Gly Gln Thr Val Thr Asn Lys Val Asp Gly Leu  
1130 1135 1140

Pro Asp Gly Val Thr Phe Asp Glu Thr Thr Asn Thr Ile Ser Gly  
1145 1150 1155

Thr Pro Ser Lys Val Gly Ser Tyr Asp Ile Thr Val Thr Thr Thr  
1160 1165 1170

Asp Glu Ser Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Glu Val  
1175 1180 1185

Glu Asp Thr Thr Lys Pro Thr Val Glu Asn Val Ala Gly Gln Thr  
1190 1195 1200

Gln Glu Ile Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr  
1205 1210 1215

Asp Asn Ser Gly Gln Ala Val Thr Asn Lys Val Glu Gly Leu Pro  
1220 1225 1230

Ala Gly Val Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr  
1235 1240 1245

Pro Ser Glu Val Gly Ser Tyr Thr Val Thr Val Thr Thr Met Asp  
1250 1255 1260

Glu Ser Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Asp Val Glu  
1265 1270 1275

Asp Thr Thr Lys Pro Thr Val Glu Ser Val Ala Asp Gln Thr Gln  
1280 1285 1290

Glu Val Asn Thr Glu Ile Thr Pro Ile Thr Ile Glu Ser Glu Asp  
1295 1300 1305

Asn Ser Asp Gln Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asp  
1310 1315 1320

Gly Val Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro  
1325 1330 1335

Ser Glu Val Gly Ser Tyr Thr Val Thr Val Thr Thr Asp Glu  
1340 1345 1350

Ser Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Asp Val Glu Asp  
1355 1360 1365

Thr Thr Lys Pro Thr Val Lys Ser Val Ser Asp Gln Thr Gln Glu  
1370 1375 1380

Val Asn Thr Glu Ile Thr Pro Ile Lys Ile Glu Ala Thr Asp Asn  
1385 1390 1395

Ser Gly Gln Thr Val Thr Asn Lys Val Asp Gly Leu Pro Asp Gly

1400 1405 1410  
Ile Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser  
1415 1420 1425  
Glu Val Gly Ser Tyr Asp Ile Thr Val Thr Thr Thr Asp Glu Ser  
1430 1435 1440  
Gly Asn Ala Thr Glu Thr Thr Phe Thr Ile Asn Val Glu Asp Thr  
1445 1450 1455  
Thr Lys Pro Thr Val Glu Asp Ile Ala Asp Gln Thr Gln Glu Val  
1460 1465 1470  
Asn Thr Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr Asp Asn Gly  
1475 1480 1485  
Gly Gln Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asp Gly Val  
1490 1495 1500  
Thr Phe Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu  
1505 1510 1515  
Val Gly Ser Tyr Asp Ile Ile Val Thr Thr Thr Asp Glu Asn Gly  
1520 1525 1530  
Asn Ser Glu Thr Thr Phe Thr Ile Asp Val Glu Asp Thr Thr  
1535 1540 1545  
Lys Pro Thr Val Glu Ser Val Val Asp Gln Thr Gln Glu Val Asn  
1550 1555 1560  
Thr Glu Ile Thr Pro Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly  
1565 1570 1575  
Gln Ala Val Ala Asn Lys Val Asp Gly Leu Pro Asn Gly Val Thr  
1580 1585 1590  
Phe Asp Glu Thr Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val  
1595 1600 1605  
Gly Ser Tyr Asp Ile Ile Val Thr Thr Thr Asp Glu Ser Gly Asn  
1610 1615 1620

Val Thr Glu Thr Ile Phe Thr Ile Asp Val Glu Asp Thr Thr Lys  
1625 1630 1635

Pro Thr Val Glu Ser Ile Ala Gly Gln Thr Gln Glu Val Asn Thr  
1640 1645 1650

Glu Ile Glu Pro Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln  
1655 1660 1665

Ala Val Thr Asn Lys Val Asp Gly Leu Pro Asn Gly Val Thr Phe  
1670 1675 1680

Asp Glu Ala Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly  
1685 1690 1695

Ile Tyr Thr Val Thr Val Thr Thr Thr Asp Glu Ser Gly Asn Ala  
1700 1705 1710

Thr Glu Thr Thr Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro  
1715 1720 1725

Thr Val Glu Ser Val Ala Asp Gln Thr Gln Glu Val Asn Thr Glu  
1730 1735 1740

Ile Thr Pro Ile Thr Ile Glu Ser Glu Asp Asn Ser Gly Gln Ala  
1745 1750 1755

Val Thr Asn Lys Val Glu Gly Leu Pro Ala Gly Met Thr Phe Asp  
1760 1765 1770

Glu Thr Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser  
1775 1780 1785

Tyr Thr Val Thr Val Thr Thr Asp Glu Ser Gly Asn Glu Thr  
1790 1795 1800

Glu Thr Thr Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro Thr  
1805 1810 1815

Val Glu Ser Ile Ala Asn Gln Thr Gln Glu Val Asn Thr Glu Ile  
1820 1825 1830

Thr Pro Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln Ala Val  
1835 1840 1845

Thr Asn Lys Val Asp Gly Leu Pro Asn Gly Val Thr Phe Asp Glu  
1850 1855 1860

Thr Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr  
1865 1870 1875

Asp Ile Lys Val Thr Thr Asp Glu Ser Gly Asn Ala Thr Glu  
1880 1885 1890

Thr Thr Phe Thr Ile Asn Val Glu Asp Thr Thr Lys Pro Thr Val  
1895 1900 1905

Glu Ser Val Ala Asp Gln Thr Gln Glu Ile Asn Thr Glu Ile Glu  
1910 1915 1920

Pro Ile Lys Ile Glu Ala Arg Asp Asn Ser Gly Gln Ala Val Thr  
1925 1930 1935

Asn Lys Val Asp Gly Leu Pro Asp Gly Val Thr Phe Asp Glu Ala  
1940 1945 1950

Thr Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Ser Tyr Asp  
1955 1960 1965

Ile Thr Val Thr Thr Asp Glu Ser Gly Asn Ala Thr Glu Thr  
1970 1975 1980

Thr Phe Thr Ile Asp Val Glu Asp Thr Thr Lys Pro Thr Val Glu  
1985 1990 1995

Asp Ile Thr Asp Gln Thr Gln Glu Ile Asn Thr Glu Met Thr Pro  
2000 2005 2010

Ile Lys Ile Glu Ala Thr Asp Asn Ser Gly Gln Ala Val Thr Asn  
2015 2020 2025

Lys Val Glu Gly Leu Pro Asp Gly Val Thr Phe Asp Glu Ala Thr  
2030 2035 2040

Asn Thr Ile Ser Gly Thr Pro Ser Glu Val Gly Lys Tyr Leu Ile  
2045 2050 2055

Thr Ile Thr Thr Ile Asp Lys Asp Gly Asn Thr Ala Thr Thr Thr  
2060 2065 2070

Leu Thr Ile Asn Val Ile Asp Thr Thr Thr Pro Glu Gln Pro Thr  
2075 2080 2085

Ile Asn Lys Val Thr Glu Asn Ser Thr Glu Val Asn Gly Arg Gly  
2090 2095 2100

Glu Pro Gly Thr Val Val Glu Val Thr Phe Pro Asp Gly Asn Lys  
2105 2110 2115

Val Glu Gly Lys Val Asp Ser Asp Gly Asn Tyr His Ile Gln Ile  
2120 2125 2130

Pro Ser Glu Thr Thr Leu Lys Gly Gly Gln Pro Leu Gln Val Ile  
2135 2140 2145

Ala Ile Asp Lys Ala Gly Asn Lys Ser Glu Ala Thr Thr Thr Asn  
2150 2155 2160

Val Ile Asp Thr Thr Ala Pro Glu Gln Pro Thr Ile Asn Lys Val  
2165 2170 2175

Thr Glu Asn Ser Thr Glu Val Ser Gly Arg Gly Glu Pro Gly Thr  
2180 2185 2190

Val Val Glu Val Thr Phe Pro Asp Gly Asn Lys Val Glu Gly Lys  
2195 2200 2205

Val Asp Ser Asp Gly Asn Tyr His Ile Gln Ile Pro Ser Asp Glu  
2210 2215 2220

Arg Phe Lys Val Gly Gln Gln Leu Ile Val Lys Val Val Asp Glu  
2225 2230 2235

Glu Gly Asn Val Ser Glu Pro Ser Ile Thr Met Val Gln Lys Glu  
2240 2245 2250

Asp Lys Asn Ser Glu Lys Leu Ser Thr Val Thr Gly Thr Val Thr

2255

2260

2265

Lys Asn Asn Ser Lys Ser Leu Lys His Lys Ala Ser Glu Gln Gln  
2270 2275 2280

Ser Tyr His Asn Lys Ser Glu Lys Ile Lys Asn Val Asn Lys Pro  
2285 2290 2295

Thr Lys Ile Val Glu Lys Asp Met Ser Thr Tyr Asp Tyr Ser Arg  
2300 2305 2310

Tyr Ser Lys Asp Ile Ser Asn Lys Asn Asn Lys Ser Ala Thr Phe  
2315 2320 2325

Glu Gln Gln Asn Val Ser Asp Ile Asn Asn Asn Gln Tyr Ser Arg  
2330 2335 2340

Asn Lys Val Asn Gln Pro Val Lys Lys Ser Arg Lys Asn Glu Ile  
2345 2350 2355

Asn Lys Asp Leu Pro Gln Thr Gly Glu Glu Asn Phe Asn Lys Ser  
2360 2365 2370

Thr Leu Phe Gly Thr Leu Val Ala Ser Leu Gly Ala Leu Leu Leu  
2375 2380 2385

Phe Phe Lys Arg Arg Lys Lys Asp Glu Asn Asp Glu Lys Glu  
2390 2395 2400

<210> 21

<211> 892

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 21

Leu Phe Gly Leu Gly His Asn Glu Ala Lys Ala Glu Glu Asn Thr Val  
1 5 10 15

Gln Asp Val Lys Asp Ser Asn Met Asp Asp Glu Leu Ser Asp Ser Asn  
20 25 30

Asp Gln Ser Ser Asn Glu Glu Lys Asn Asp Val Ile Asn Asn Ser Gln  
35 40 45

Ser Ile Asn Thr Asp Asp Asn Gln Ile Lys Lys Glu Glu Thr Asn  
50 55 60

Ser Asn Asp Ala Ile Glu Asn Arg Ser Lys Asp Ile Thr Gln Ser Thr  
65 70 75 80

Thr Asn Val Asp Glu Asn Glu Ala Thr Phe Leu Gln Lys Thr Pro Gln  
85 90 95

Asp Asn Thr Gln Leu Lys Glu Glu Val Val Lys Glu Pro Ser Ser Val  
100 105 110

Glu Ser Ser Asn Ser Ser Met Asp Thr Ala Gln Gln Pro Ser His Thr  
115 120 125

Thr Ile Asn Ser Glu Ala Ser Ile Gln Thr Ser Asp Asn Glu Glu Asn  
130 135 140

Ser Arg Val Ser Asp Phe Ala Asn Ser Lys Ile Ile Glu Ser Asn Thr  
145 150 155 160

Glu Ser Asn Lys Glu Glu Asn Thr Ile Glu Gln Pro Asn Lys Val Arg  
165 170 175

Glu Asp Ser Ile Thr Ser Gln Pro Ser Ser Tyr Lys Asn Ile Asp Glu  
180 185 190

Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn Leu Pro Ile Asn Glu Tyr  
195 200 205

Glu Asn Lys Val Arg Pro Leu Ser Thr Thr Ser Ala Gln Pro Ser Ser  
210 215 220

Lys Arg Val Thr Val Asn Gln Leu Ala Ala Glu Gln Gly Ser Asn Val  
225 230 235 240

Asn His Leu Ile Lys Val Thr Asp Gln Ser Ile Thr Glu Gly Tyr Asp  
245 250 255

Asp Ser Asp Gly Ile Ile Lys Ala His Asp Ala Glu Asn Leu Ile Tyr  
260 265 270

Asp Val Thr Phe Glu Val Asp Asp Lys Val Lys Ser Gly Asp Thr Met  
275 280 285

Thr Val Asn Ile Asp Lys Asn Thr Val Pro Ser Asp Leu Thr Asp Ser  
290 295 300

Phe Ala Ile Pro Lys Ile Lys Asp Asn Ser Gly Glu Ile Ile Ala Thr  
305 310 315 320

Gly Thr Tyr Asp Asn Thr Asn Lys Gln Ile Thr Tyr Thr Phe Thr Asp  
325 330 335

Tyr Val Asp Lys Tyr Glu Asn Ile Lys Ala His Leu Lys Leu Thr Ser  
340 345 350

Tyr Ile Asp Lys Ser Lys Val Pro Asn Asn Asn Thr Lys Leu Asp Val  
355 360 365

Glu Tyr Lys Thr Ala Leu Ser Ser Val Asn Lys Thr Ile Thr Val Glu  
370 375 380

Tyr Gln Lys Pro Asn Glu Asn Arg Thr Ala Asn Leu Gln Ser Met Phe  
385 390 395 400

Thr Asn Ile Asp Thr Lys Asn His Thr Val Glu Gln Thr Ile Tyr Ile  
405 410 415

Asn Pro Leu Arg Tyr Ser Ala Lys Glu Thr Asn Val Asn Ile Ser Gly  
420 425 430

Asn Gly Asp Glu Gly Ser Thr Ile Ile Asp Asp Ser Thr Ile Ile Lys  
435 440 445

Val Tyr Lys Val Gly Asp Asn Gln Asn Leu Pro Asp Ser Asn Arg Ile  
450 455 460

Tyr Asp Tyr Ser Glu Tyr Glu Asp Val Thr Asn Asp Asp Tyr Ala Gln  
465 470 475 480

Leu Gly Asn Asn Asn Asp Val Asn Ile Asn Phe Gly Asn Ile Asp Ser  
485 490 495

Pro Tyr Ile Ile Lys Val Ile Ser Lys Tyr Asp Pro Asn Lys Asp Asp

500

505

510

Tyr Thr Thr Ile Gln Gln Thr Val Thr Met Gln Thr Thr Ile Asn Glu  
515 520 525

Tyr Thr Gly Glu Phe Arg Thr Ala Ser Tyr Asp Asn Thr Ile Ala Phe  
530 535 540

Ser Thr Ser Ser Gly Gln Gly Gln Gly Asp Leu Pro Pro Glu Lys Thr  
545 550 555 560

Tyr Lys Ile Gly Asp Tyr Val Trp Glu Asp Val Asp Lys Asp Gly Ile  
565 570 575

Gln Asn Thr Asn Asp Asn Glu Lys Pro Leu Ser Asn Val Leu Val Thr  
580 585 590

Leu Thr Tyr Pro Asp Gly Thr Ser Lys Ser Val Arg Thr Asp Glu Glu  
595 600 605

Gly Lys Tyr Gln Phe Asp Gly Leu Lys Asn Gly Leu Thr Tyr Lys Ile  
610 615 620

Thr Phe Glu Thr Pro Glu Gly Tyr Thr Pro Thr Leu Lys His Ser Gly  
625 630 635 640

Thr Asn Pro Ala Leu Asp Ser Glu Gly Asn Ser Val Trp Val Thr Ile  
645 650 655

Asn Gly Gln Asp Asp Met Thr Ile Asp Ser Gly Phe Tyr Gln Thr Pro  
660 665 670

Lys Tyr Ser Leu Gly Asn Tyr Val Trp Tyr Asp Thr Asn Lys Asp Gly  
675 680 685

Ile Gln Gly Asp Asp Glu Lys Gly Ile Ser Gly Val Lys Val Thr Leu  
690 695 700

Lys Asp Glu Asn Gly Asn Ile Ile Ser Thr Thr Thr Asp Glu Asn  
705 710 715 720

Gly Lys Tyr Gln Phe Asp Asn Leu Asn Ser Gly Asn Tyr Ile Val His  
725 730 735

Phe Asp Lys Pro Ser Gly Met Thr Gln Thr Thr Thr Asp Ser Gly Asp  
740 745 750

Asp Asp Glu Gln Asp Ala Asp Gly Glu Glu Val His Val Thr Ile Thr  
755 760 765

Asp His Asp Asp Phe Ser Ile Asp Asn Gly Tyr Tyr Asp Asp Asp Ser  
770 775 780

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Asp Ser Asp Ser Asp  
785 790 795 800

Ser Asp  
805 810 815

Ser Asp  
820 825 830

Ser Asp Ser Asp Ser Asp Ser Gly Leu Asp Asn Ser Ser Asp Lys Asn  
835 840 845

Thr Lys Asp Lys Leu Pro Asp Thr Gly Ala Asn Glu Asp His Asp Ser  
850 855 860

Lys Gly Thr Leu Leu Gly Ala Leu Phe Ala Gly Leu Gly Ala Leu Leu  
865 870 875 880

Leu Gly Lys Arg Arg Lys Asn Arg Lys Asn Lys Asn  
885 890

<210> 22

<211> 1973

<212> PRT

<213> Staphylococcus epidermidis

<400> 22

Met Lys Glu Asn Lys Arg Lys Asn Asn Leu Asp Lys Asn Asn Thr Arg  
1 5 10 15

Phe Ser Ile Arg Lys Tyr Gln Gly Tyr Gly Ala Thr Ser Val Ala Ile  
20 25 30

Ile Gly Phe Ile Ile Ser Cys Phe Ser Glu Ala Lys Ala Asp Ser  
35 40 45

Asp Lys His Glu Ile Lys Ser His Gln Gln Ser Met Thr Asn His Leu  
50 55 60

Thr Thr Leu Pro Ser Asp Asn Gln Glu Asn Thr Ser Asn Asn Glu Phe  
65 70 75 80

Asn Asn Arg Asn His Asp Ile Ser His Leu Ser Leu Asn Lys Ser Ile  
85 90 95

Gln Met Asp Glu Leu Lys Leu Ile Lys Gln Tyr Lys Ala Ile Asn  
100 105 110

Leu Asn Asp Lys Thr Glu Glu Ser Ile Lys Leu Phe Gln Ser Asp Leu  
115 120 125

Val Gln Ala Glu Ser Leu Ile Asn Asn Pro Gln Ser Gln Gln His Val  
130 135 140

Asp Ala Phe Tyr His Lys Phe Leu Asn Ser Ala Gly Lys Leu Arg Lys  
145 150 155 160

Lys Glu Thr Val Ser Ile Lys His Glu Arg Ser Glu Ser Asn Thr Tyr  
165 170 175

Arg Leu Gly Asp Glu Val Arg Ser Gln Thr Phe Ser His Ile Arg His  
180 185 190

Lys Arg Asn Ala Val Ser Phe Arg Asn Ala Asp Gln Ser Asn Leu Ser  
195 200 205

Thr Asp Pro Leu Lys Ala Asn Glu Ile Asn Pro Glu Ile Gln Asn Gly  
210 215 220

Asn Phe Ser Gln Val Ser Gly Gly Pro Leu Pro Thr Ser Ser Lys Arg  
225 230 235 240

Leu Thr Val Val Thr Asn Val Asp Asn Trp His Ser Tyr Ser Thr Asp  
245 250 255

Pro Asn Pro Glu Tyr Pro Met Phe Tyr Thr Thr Ala Val Asn Tyr

260

265

270

Pro Asn Phe Met Ser Asn Gly Asn Ala Pro Tyr Gly Val Ile Leu Gly  
275 280 285

Arg Thr Thr Asp Gly Trp Asn Arg Asn Val Ile Asp Ser Lys Val Ala  
290 295 300

Gly Ile Tyr Gln Asp Ile Asp Val Val Pro Gly Ser Glu Leu Asn Val  
305 310 315 320

Asn Phe Ile Ser Thr Ser Pro Val Phe Ser Asp Gly Ala Ala Gly Ala  
325 330 335

Lys Leu Lys Ile Ser Asn Val Glu Gln Asn Arg Val Leu Phe Asp Ser  
340 345 350

Arg Leu Asn Gly Met Gly Pro Tyr Pro Thr Gly Lys Leu Ser Ala Met  
355 360 365

Val Asn Ile Pro Asn Asp Ile Asn Arg Val Arg Ile Ser Phe Leu Pro  
370 375 380

Val Ser Ser Thr Gly Arg Val Ser Val Gln Arg Ser Ser Arg Glu His  
385 390 395 400

Gly Phe Gly Asp Asn Ser Ser Tyr Tyr His Gly Gly Ser Val Ser Asp  
405 410 415

Val Arg Ile Asn Ser Gly Ser Tyr Val Val Ser Lys Val Thr Gln Arg  
420 425 430

Glu Tyr Thr Thr Arg Pro Asn Ser Ser Asn Asp Thr Phe Ala Arg Ala  
435 440 445

Thr Ile Asn Leu Ser Val Glu Asn Lys Gly His Asn Gln Ser Lys Asp  
450 455 460

Thr Tyr Tyr Glu Val Ile Leu Pro Gln Asn Ser Arg Leu Ile Ser Thr  
465 470 475 480

Arg Gly Gly Ser Gly Asn Tyr Asn Asn Ala Thr Asn Lys Leu Ser Ile  
485 490 495

Arg Leu Asp Asn Leu Asn Pro Gly Asp Arg Arg Asp Ile Ser Tyr Thr  
500 505 510

Val Asp Phe Glu Ser Ser Ser Pro Lys Leu Ile Asn Leu Asn Ala His  
515 520 525

Leu Leu Tyr Lys Thr Asn Ala Thr Phe Arg Gly Asn Asp Gly Gln Arg  
530 535 540

Thr Gly Asp Asn Ile Val Asp Leu Gln Ser Ile Ala Leu Leu Met Asn  
545 550 555 560

Lys Asp Val Leu Glu Thr Glu Leu Asn Glu Ile Asp Lys Phe Ile Arg  
565 570 575

Asp Leu Asn Glu Ala Asp Phe Thr Ile Asp Ser Trp Ser Ala Leu Gln  
580 585 590

Glu Lys Met Thr Glu Gly Gly Asn Ile Leu Asn Glu Gln Gln Asn Gln  
595 600 605

Val Ala Leu Glu Asn Gln Ala Ser Gln Glu Thr Ile Asn Asn Val Thr  
610 615 620

Gln Ser Leu Glu Ile Leu Lys Asn Asn Leu Lys Tyr Lys Thr Pro Ser  
625 630 635 640

Gln Pro Ile Ile Lys Ser Asn Asn Gln Ile Pro Asn Ile Thr Ile Ser  
645 650 655

Pro Ala Asp Lys Ala Asp Lys Leu Thr Ile Thr Tyr Gln Asn Thr Asp  
660 665 670

Asn Glu Ser Ala Ser Ile Ile Gly Asn Lys Leu Asn Asn Gln Trp Ser  
675 680 685

Leu Asn Asn Asn Ile Pro Gly Ile Glu Ile Asp Met Gln Thr Gly Leu  
690 695 700

Val Thr Ile Asp Tyr Lys Ala Val Tyr Pro Glu Ser Val Val Gly Ala  
705 710 715 720

Asn Asp Lys Thr Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr  
725 730 735

Met Pro Arg Lys Glu Ala Thr Pro Leu Ser Pro Ile Val Glu Ala Asn  
740 745 750

Glu Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln  
755 760 765

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu Val  
770 775 780

Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile Asp Tyr  
785 790 795 800

Val Asn Ile Glu Glu Asn Ser Gly Lys Val Thr Ile Gly Tyr Gln Ala  
805 810 815

Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr Lys Gly Asn Ser  
820 825 830

Asp Glu Ser Ala Glu Ser Arg Val Thr Met Pro Arg Lys Glu Ala Thr  
835 840 845

Pro His Ser Pro Ile Val Glu Ala Asn Glu Glu His Val Asn Val Thr  
850 855 860

Ile Ala Pro Asn Gly Glu Ala Thr Gln Ile Ala Ile Lys Tyr Arg Thr  
865 870 875 880

Pro Asp Gly Gln Glu Thr Thr Leu Ile Ala Ser Lys Asn Gly Ser Ser  
885 890 895

Trp Thr Leu Asn Lys Gln Ile Asp Tyr Val Asn Ile Glu Glu Asn Ser  
900 905 910

Gly Lys Val Thr Ile Gly Tyr Gln Ala Val Gln Leu Glu Ser Glu Val  
915 920 925

Ile Ala Thr Glu Thr Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg  
930 935 940

Ile Thr Met Leu Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu  
945 950 955 960

Ala Asn Glu Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Ala  
965 970 975

Thr Gln Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr  
980 985 990

Leu Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile  
995 1000 1005

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1010 1015 1020

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr  
1025 1030 1035

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro  
1040 1045 1050

Arg Lys Glu Ala Thr Pro Ile Pro Pro Thr Leu Glu Ala Ser Val  
1055 1060 1065

Gln Glu Ala Ser Val Thr Val Thr Pro Asn Glu Asn Ala Thr Lys  
1070 1075 1080

Val Phe Ile Lys Tyr Leu Asp Ile Asn Asp Glu Ile Ser Thr Ile  
1085 1090 1095

Ile Ala Ser Lys Ile Asn Gln Gln Trp Thr Leu Asn Lys Asp Asn  
1100 1105 1110

Phe Gly Ile Lys Ile Asn Pro Leu Thr Gly Lys Val Ile Ile Ser  
1115 1120 1125

Tyr Val Ala Val Gln Pro Glu Ser Asp Val Ile Ala Ile Glu Ser  
1130 1135 1140

Gln Gly Asn Ser Asp Leu Ser Glu Glu Ser Arg Ile Ile Met Pro  
1145 1150 1155

Thr Lys Glu Glu Pro Pro Glu Pro Pro Ile Leu Glu Ser Asp Ser

1160

1165

1170

Ile Glu Ala Lys Val Asn Ile Phe Pro Asn Asp Glu Ala Thr Arg  
1175 1180 1185

Ile Val Ile Met Tyr Thr Ser Leu Glu Gly Gln Glu Ala Thr Leu  
1190 1195 1200

Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile  
1205 1210 1215

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1220 1225 1230

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr  
1235 1240 1245

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Val Thr Met Pro  
1250 1255 1260

Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu Thr Asn Glu  
1265 1270 1275

Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln  
1280 1285 1290

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Thr Thr Leu  
1295 1300 1305

Ile Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile  
1310 1315 1320

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1325 1330 1335

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr  
1340 1345 1350

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro  
1355 1360 1365

Arg Lys Glu Ala Ile Pro His Ser Pro Ile Val Glu Ala Asn Glu  
1370 1375 1380

Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Thr Thr Gln  
1385 1390 1395

Ile Ala Val Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu  
1400 1405 1410

Ile Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile  
1415 1420 1425

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1430 1435 1440

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr  
1445 1450 1455

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro  
1460 1465 1470

Val Lys Glu Lys Thr Pro Ala Pro Pro Ile Ser Ile Ile Asn Glu  
1475 1480 1485

Ser Asn Ala Ser Val Glu Ile Ile Pro Gln Val Asn Val Thr Gln  
1490 1495 1500

Leu Ser Leu Gln Tyr Ile Asp Ala Lys Gly Gln Gln Gln Asn Leu  
1505 1510 1515

Ile Ala Thr Leu Asn Gln Asn Gln Trp Thr Leu Asn Lys Asn Val  
1520 1525 1530

Ser His Ile Thr Val Asp Lys Asn Thr Gly Lys Val Leu Ile Asn  
1535 1540 1545

Tyr Gln Ala Val Tyr Pro Glu Ser Glu Val Ile Ala Arg Glu Ser  
1550 1555 1560

Lys Gly Asn Ser Asp Ser Ser Asn Val Ser Met Val Ile Met Pro  
1565 1570 1575

Arg Lys Thr Ala Thr Pro Lys Pro Pro Ile Ile Lys Val Asp Glu  
1580 1585 1590

Met Asn Ala Ser Leu Ala Ile Ile Pro Tyr Lys Asn Asn Thr Ala  
1595 1600 1605

Ile Asn Ile His Tyr Ile Asp Lys Lys Gly Ile Lys Ser Met Val  
1610 1615 1620

Thr Ala Ile Lys Asn Asn Asp Gln Trp Gln Leu Asp Glu Lys Ile  
1625 1630 1635

Lys Tyr Val Lys Ile Asp Ala Lys Thr Gly Thr Val Ile Ile Asn  
1640 1645 1650

Tyr Gln Ile Val Gln Glu Asn Ser Glu Ile Ile Ala Thr Ala Ile  
1655 1660 1665

Asn Gly Asn Ser Asp Lys Ser Glu Glu Val Lys Val Leu Met Pro  
1670 1675 1680

Ile Lys Glu Phe Thr Pro Leu Ala Pro Leu Leu Glu Thr Asn Tyr  
1685 1690 1695

Lys Lys Ala Thr Val Ser Ile Leu Pro Gln Ser Asn Ala Thr Lys  
1700 1705 1710

Leu Asp Phe Lys Tyr Arg Asp Lys Lys Gly Asp Ser Lys Ile Ile  
1715 1720 1725

Ile Val Lys Arg Phe Lys Asn Ile Trp Lys Ala Asn Glu Gln Ile  
1730 1735 1740

Ser Gly Val Thr Ile Asn Pro Glu Phe Gly Gln Val Val Ile Asn  
1745 1750 1755

Tyr Gln Ala Val Tyr Pro Glu Ser Asp Ile Leu Ala Ala Gln Tyr  
1760 1765 1770

Val Gly Asn Ser Asp Ala Ser Glu Trp Ala Lys Val Lys Met Pro  
1775 1780 1785

Lys Lys Glu Leu Ala Pro His Ser Pro Ser Leu Ile Tyr Asp Asn  
1790 1795 1800

Arg Asn Asn Lys Ile Leu Ile Ala Pro Asn Ser Asn Ala Thr Glu  
1805 1810 1815

Met Glu Leu Ser Tyr Val Asp Lys Asn Asn Gln Ser Leu Lys Val  
1820 1825 1830

Lys Ala Leu Lys Ile Asn Asn Arg Trp Lys Phe Asp Ser Ser Val  
1835 1840 1845

Ser Asn Ile Ser Ile Asn Pro Asn Thr Gly Lys Ile Val Leu Gln  
1850 1855 1860

Pro Gln Phe Leu Leu Thr Asn Ser Lys Ile Ile Val Phe Ala Lys  
1865 1870 1875

Lys Gly Asn Ser Asp Ala Ser Ile Ser Val Ser Leu Arg Val Pro  
1880 1885 1890

Ala Val Lys Lys Ile Glu Leu Glu Pro Met Phe Asn Val Pro Val  
1895 1900 1905

Leu Val Ser Leu Asn Lys Lys Arg Ile Gln Phe Asp Asp Cys Ser  
1910 1915 1920

Gly Val Lys Asn Cys Leu Asn Lys Gln Ile Ser Lys Thr Gln Leu  
1925 1930 1935

Pro Asp Thr Gly Tyr Ser Asp Lys Ala Ser Lys Ser Asn Ile Leu  
1940 1945 1950

Ser Val Leu Leu Leu Gly Phe Gly Phe Leu Ser Tyr Ser Arg Lys  
1955 1960 1965

Arg Lys Glu Lys Gln  
1970

<210> 23  
<211> 10203  
<212> PRT  
<213> *Staphylococcus epidermidis*

<400> 23

Met Lys Ser Lys Pro Lys Leu Asn Gly Arg Asn Ile Cys Ser Phe Leu  
1 5 10 15

Leu Ser Lys Cys Met Ser Tyr Ser Leu Ser Lys Leu Ser Thr Leu Lys  
20 25 30

Thr Tyr Asn Phe Gln Ile Thr Ser Asn Asn Lys Glu Lys Thr Ser Arg  
35 40 45

Ile Gly Val Ala Ile Ala Leu Asn Asn Arg Asp Lys Leu Gln Lys Phe  
50 55 60

Ser Ile Arg Lys Tyr Ala Ile Gly Thr Phe Ser Thr Val Ile Ala Thr  
65 70 75 80

Leu Val Phe Met Gly Ile Asn Thr Asn His Ala Ser Ala Asp Glu Leu  
85 90 95

Asn Gln Asn Gln Lys Leu Ile Lys Gln Leu Asn Gln Thr Asp Asp Asp  
100 105 110

Asp Ser Asn Thr His Ser Gln Glu Ile Glu Asn Asn Lys Gln Asn Ser  
115 120 125

Ser Gly Lys Thr Glu Ser Leu Arg Ser Ser Thr Ser Gln Asn Gln Ala  
130 135 140

Asn Ala Arg Leu Ser Asp Gln Phe Lys Asp Thr Asn Glu Thr Ser Gln  
145 150 155 160

Gln Leu Pro Thr Asn Val Ser Asp Asp Ser Ile Asn Gln Ser His Ser  
165 170 175

Glu Ala Asn Met Asn Asn Glu Pro Leu Lys Val Asp Asn Ser Thr Met  
180 185 190

Gln Ala His Ser Lys Ile Val Ser Asp Ser Asp Gly Asn Ala Ser Glu  
195 200 205

Asn Lys His His Lys Leu Thr Glu Asn Val Leu Ala Glu Ser Arg Ala  
210 215 220

Ser Lys Asn Asp Lys Glu Lys Glu Asn Leu Gln Glu Lys Asp Lys Ser  
225 230 235 240

Gln Gln Val His Pro Pro Leu Asp Lys Asn Ala Leu Gln Ala Phe Phe  
245 250 255

Asp Ala Ser Tyr His Asn Tyr Arg Met Ile Asp Arg Asp Arg Ala Asp  
260 265 270

Ala Thr Glu Tyr Gln Lys Val Lys Ser Thr Phe Asp Tyr Val Asn Asp  
275 280 285

Leu Leu Gly Asn Asn Gln Asn Ile Pro Ser Glu Gln Leu Val Ser Ala  
290 295 300

Tyr Gln Gln Leu Glu Lys Ala Leu Glu Leu Ala Arg Thr Leu Pro Gln  
305 310 315 320

Gln Ser Thr Thr Glu Lys Arg Gly Arg Arg Ser Thr Arg Ser Val Val  
325 330 335

Glu Asn Arg Ser Ser Arg Ser Asp Tyr Leu Asp Ala Arg Thr Glu Tyr  
340 345 350

Tyr Val Ser Lys Asp Asp Asp Ser Gly Phe Pro Pro Gly Thr Phe  
355 360 365

Phe His Ala Ser Asn Arg Arg Trp Pro Tyr Asn Leu Pro Arg Ser Arg  
370 375 380

Asn Ile Leu Arg Ala Ser Asp Val Gln Gly Asn Ala Tyr Ile Thr Thr  
385 390 395 400

Lys Arg Leu Lys Asp Gly Tyr Gln Trp Asp Ile Leu Phe Asn Ser Asn  
405 410 415

His Lys Gly His Glu Tyr Met Tyr Tyr Trp Phe Gly Leu Pro Ser Asp  
420 425 430

Gln Thr Pro Thr Gly Pro Val Thr Phe Thr Ile Ile Asn Arg Asp Gly  
435 440 445

Ser Ser Thr Ser Thr Gly Gly Val Gly Phe Gly Ser Gly Ala Pro Leu  
450 455 460

Pro Gln Phe Trp Arg Ser Ala Gly Ala Ile Asn Ser Ser Val Ala Asn  
465 470 475 480

Asp Phe Lys His Gly Ser Ala Thr Asn Tyr Ala Phe Tyr Asp Gly Val  
485 490 495

Asn Asn Phe Ser Asp Phe Ala Arg Gly Gly Glu Leu Tyr Phe Asp Arg  
500 505 510

Glu Gly Ala Thr Gln Thr Asn Lys Tyr Tyr Gly Asp Glu Asn Phe Ala  
515 520 525

Leu Leu Asn Ser Glu Lys Pro Asp Gln Ile Arg Gly Leu Asp Thr Ile  
530 535 540

Tyr Ser Phe Lys Gly Ser Gly Asp Val Ser Tyr Arg Ile Ser Phe Lys  
545 550 555 560

Thr Gln Gly Ala Pro Thr Ala Arg Leu Tyr Tyr Ala Ala Gly Ala Arg  
565 570 575

Ser Gly Glu Tyr Lys Gln Ala Thr Asn Tyr Asn Gln Leu Tyr Val Glu  
580 585 590

Pro Tyr Lys Asn Tyr Arg Asn Arg Val Gln Ser Asn Val Gln Val Lys  
595 600 605

Asn Arg Thr Leu His Leu Lys Arg Thr Ile Arg Gln Phe Asp Pro Thr  
610 615 620

Leu Gln Arg Thr Thr Asp Val Pro Ile Leu Asp Ser Asp Gly Ser Gly  
625 630 635 640

Ser Ile Asp Ser Val Tyr Asp Pro Leu Ser Tyr Val Lys Asn Val Thr  
645 650 655

Gly Thr Val Leu Gly Ile Tyr Pro Ser Tyr Leu Pro Tyr Asn Gln Glu  
660 665 670

Arg Trp Gln Gly Ala Asn Ala Met Asn Ala Tyr Gln Ile Glu Glu Leu  
675 680 685

Phe Ser Gln Glu Asn Leu Gln Asn Ala Ala Arg Ser Gly Arg Pro Ile

690

695

700

Gln Phe Leu Val Gly Phe Asp Val Glu Asp Ser His His Asn Pro Glu  
705 710 715 720

Thr Leu Leu Pro Val Asn Leu Tyr Val Lys Pro Glu Leu Lys His Thr  
725 730 735

Ile Glu Leu Tyr His Asp Asn Glu Lys Gln Asn Arg Lys Glu Phe Ser  
740 745 750

Val Ser Lys Arg Ala Gly His Gly Val Phe Gln Ile Met Ser Gly Thr  
755 760 765

Leu His Asn Thr Val Gly Ser Gly Ile Leu Pro Tyr Gln Gln Glu Ile  
770 775 780

Arg Ile Lys Leu Thr Ser Asn Glu Pro Ile Lys Asp Ser Glu Trp Ser  
785 790 795 800

Ile Thr Gly Tyr Pro Asn Thr Leu Thr Leu Gln Asn Ala Val Gly Arg  
805 810 815

Thr Asn Asn Ala Thr Glu Lys Asn Leu Ala Leu Val Gly His Ile Asp  
820 825 830

Pro Gly Asn Tyr Phe Ile Thr Val Lys Phe Gly Asp Lys Val Glu Gln  
835 840 845

Phe Glu Ile Arg Ser Lys Pro Thr Pro Pro Arg Ile Ile Thr Thr Ala  
850 855 860

Asn Glu Leu Arg Gly Asn Ser Asn His Lys Pro Glu Ile Arg Val Thr  
865 870 875 880

Asp Ile Pro Asn Asp Thr Thr Ala Lys Ile Lys Leu Val Met Gly Gly  
885 890 895

Thr Asp Gly Asp His Asp Pro Glu Ile Asn Pro Tyr Thr Val Pro Glu  
900 905 910

Asn Tyr Thr Val Val Ala Glu Ala Tyr His Asp Asn Asp Pro Ser Lys  
915 920 925

Asn Gly Val Leu Thr Phe Arg Ser Ser Asp Tyr Leu Lys Asp Leu Pro  
930 935 940

Leu Ser Gly Glu Leu Lys Ala Ile Val Tyr Tyr Asn Gln Tyr Val Gln  
945 950 955 960

Ser Asn Phe Ser Asn Ser Val Pro Phe Ser Ser Asp Thr Thr Pro Pro  
965 970 975

Thr Ile Asn Glu Pro Ala Gly Leu Val His Lys Tyr Tyr Arg Gly Asp  
980 985 990

His Val Glu Ile Thr Leu Pro Val Thr Asp Asn Thr Gly Gly Ser Gly  
995 1000 1005

Leu Arg Asp Val Asn Val Asn Leu Pro Gln Gly Trp Thr Lys Thr  
1010 1015 1020

Phe Thr Ile Asn Pro Asn Asn Asn Thr Glu Gly Thr Leu Lys Leu  
1025 1030 1035

Ile Gly Asn Ile Pro Ser Asn Glu Ala Tyr Asn Thr Thr Tyr His  
1040 1045 1050

Phe Asn Ile Thr Ala Thr Asp Asn Ser Gly Asn Thr Thr Asn Pro  
1055 1060 1065

Ala Lys Thr Phe Ile Leu Asn Val Gly Lys Leu Ala Asp Asp Leu  
1070 1075 1080

Asn Pro Val Gly Leu Ser Arg Asp Gln Leu Gln Leu Val Thr Asp  
1085 1090 1095

Pro Ser Ser Leu Ser Asn Ser Glu Arg Glu Glu Val Lys Arg Lys  
1100 1105 1110

Ile Ser Glu Ala Asn Ala Asn Ile Arg Ser Tyr Leu Leu Gln Asn  
1115 1120 1125

Asn Pro Ile Leu Ala Gly Val Asn Gly Asp Val Thr Phe Tyr Tyr  
1130 1135 1140

Arg Asp Gly Ser Val Asp Val Ile Asp Ala Glu Asn Val Ile Thr  
1145 1150 1155

Tyr Glu Pro Glu Arg Lys Ser Ile Phe Ser Glu Asn Gly Asn Thr  
1160 1165 1170

Asn Lys Lys Glu Ala Val Ile Thr Ile Ala Arg Gly Gln Asn Tyr  
1175 1180 1185

Thr Ile Gly Pro Asn Leu Arg Lys Tyr Phe Ser Leu Ser Asn Gly  
1190 1195 1200

Ser Asp Leu Pro Asn Arg Asp Phe Thr Ser Ile Ser Ala Ile Gly  
1205 1210 1215

Ser Leu Pro Ser Ser Ser Glu Ile Ser Arg Leu Asn Val Gly Asn  
1220 1225 1230

Tyr Asn Tyr Arg Val Asn Ala Lys Asn Ala Tyr His Lys Thr Gln  
1235 1240 1245

Gln Glu Leu Asn Leu Lys Leu Lys Ile Val Glu Val Asn Ala Pro  
1250 1255 1260

Thr Gly Asn Asn Arg Val Tyr Arg Val Ser Thr Tyr Asn Leu Thr  
1265 1270 1275

Asn Asp Glu Ile Asn Lys Ile Lys Gln Ala Phe Lys Ala Ala Asn  
1280 1285 1290

Ser Gly Leu Asn Leu Asn Asp Asn Asp Ile Thr Val Ser Asn Asn  
1295 1300 1305

Phe Asp His Arg Asn Val Ser Ser Val Thr Val Thr Ile Arg Lys  
1310 1315 1320

Gly Asp Leu Ile Lys Glu Phe Ser Ser Asn Leu Asn Asn Met Asn  
1325 1330 1335

Phe Leu Arg Trp Val Asn Ile Arg Asp Asp Tyr Thr Ile Ser Trp  
1340 1345 1350

Thr Ser Ser Lys Ile Gln Gly Arg Asn Thr Asp Gly Gly Leu Glu  
1355 1360 1365

Trp Ser Pro Asp His Lys Ser Leu Ile Tyr Lys Tyr Asp Ala Thr  
1370 1375 1380

Leu Gly Arg Gln Ile Asn Thr Asn Asp Val Leu Thr Leu Leu Gln  
1385 1390 1395

Ala Thr Ala Lys Asn Ser Asn Leu Arg Ser Asn Ile Asn Ser Asn  
1400 1405 1410

Glu Lys Gln Leu Ala Glu Arg Gly Ser Asn Gly Tyr Ser Lys Ser  
1415 1420 1425

Ile Ile Arg Asp Asp Gly Glu Lys Ser Tyr Leu Leu Asn Ser Asn  
1430 1435 1440

Pro Ile Gln Val Leu Asp Leu Val Glu Pro Asp Asn Gly Tyr Gly  
1445 1450 1455

Gly Arg Gln Val Ser His Ser Asn Val Ile Tyr Asn Glu Lys Asn  
1460 1465 1470

Ser Ser Ile Val Asn Gly Gln Val Pro Glu Ala Asn Gly Ala Ser  
1475 1480 1485

Ala Phe Asn Ile Asp Lys Val Val Lys Ala Asn Ala Ala Asn Asn  
1490 1495 1500

Gly Ile Met Gly Val Ile Tyr Lys Ala Gln Leu Tyr Leu Ala Pro  
1505 1510 1515

Tyr Ser Pro Lys Gly Tyr Ile Glu Lys Leu Gly Gln Asn Leu Ser  
1520 1525 1530

Asn Thr Asn Asn Val Ile Asn Val Tyr Phe Val Pro Ser Asp Lys  
1535 1540 1545

Val Asn Pro Ser Ile Thr Val Gly Asn Tyr Asp His His Thr Val  
1550 1555 1560

Tyr Ser Gly Glu Thr Phe Lys Asn Thr Ile Asn Val Asn Asp Asn

1565 1570 1575

Tyr Gly Leu Asn Thr Val Ala Ser Thr Ser Asp Ser Ala Ile Thr  
1580 1585 1590

Met Thr Arg Asn Asn Asn Glu Leu Val Gly Gln Ala Pro Asn Val  
1595 1600 1605

Thr Asn Ser Thr Asn Lys Ile Val Lys Val Lys Ala Thr Asp Lys  
1610 1615 1620

Ser Gly Asn Glu Ser Ile Val Ser Phe Thr Val Asn Ile Lys Pro  
1625 1630 1635

Leu Asn Glu Lys Tyr Arg Ile Thr Thr Ser Ser Ser Asn Gln Thr  
1640 1645 1650

Pro Val Arg Ile Ser Asn Ile Gln Asn Asn Ala Asn Leu Ser Ile  
1655 1660 1665

Glu Asp Gln Asn Arg Val Lys Ser Ser Leu Ser Met Thr Lys Ile  
1670 1675 1680

Leu Gly Thr Arg Asn Tyr Val Asn Glu Ser Asn Asn Asp Val Arg  
1685 1690 1695

Ser Gln Val Val Ser Lys Val Asn Arg Ser Gly Asn Asn Ala Thr  
1700 1705 1710

Val Asn Val Thr Thr Phe Ser Asp Gly Thr Thr Asn Thr Ile  
1715 1720 1725

Thr Val Pro Val Lys His Val Leu Leu Glu Val Val Pro Thr Thr  
1730 1735 1740

Arg Thr Thr Val Arg Gly Gln Gln Phe Pro Thr Gly Lys Gly Thr  
1745 1750 1755

Ser Pro Asn Asp Phe Phe Ser Leu Arg Thr Gly Gly Pro Val Asp  
1760 1765 1770

Ala Arg Ile Val Trp Val Asn Asn Gln Gly Pro Asp Ile Asn Ser  
1775 1780 1785

Asn Gln Ile Gly Arg Asp Leu Thr Leu His Ala Glu Ile Phe Phe  
1790 1795 1800

Asp Gly Glu Thr Thr Pro Ile Arg Lys Asp Thr Thr Tyr Lys Leu  
1805 1810 1815

Ser Gln Ser Ile Pro Lys Gln Ile Tyr Glu Thr Thr Ile Asn Gly  
1820 1825 1830

Arg Phe Asn Ser Ser Gly Asp Ala Tyr Pro Gly Asn Phe Val Gln  
1835 1840 1845

Ala Val Asn Gln Tyr Trp Pro Glu His Met Asp Phe Arg Trp Ala  
1850 1855 1860

Gln Gly Ser Gly Thr Pro Ser Ser Arg Asn Ala Gly Ser Phe Thr  
1865 1870 1875

Lys Thr Val Thr Val Val Tyr Gln Asn Gly Gln Thr Glu Asn Val  
1880 1885 1890

Asn Val Leu Phe Lys Val Lys Pro Asn Lys Pro Val Ile Asp Ser  
1895 1900 1905

Asn Ser Val Ile Ser Lys Gly Gln Leu Asn Gly Gln Gln Ile Leu  
1910 1915 1920

Val Arg Asn Val Pro Gln Asn Ala Gln Val Thr Leu Tyr Gln Ser  
1925 1930 1935

Asn Gly Thr Val Ile Pro Asn Thr Asn Thr Thr Ile Asp Ser Asn  
1940 1945 1950

Gly Ile Ala Thr Val Thr Ile Gln Gly Thr Leu Pro Thr Gly Asn  
1955 1960 1965

Ile Thr Ala Lys Thr Ser Met Thr Asn Asn Val Thr Tyr Thr Lys  
1970 1975 1980

Gln Asn Ser Ser Gly Ile Ala Ser Asn Thr Thr Glu Asp Ile Ser  
1985 1990 1995

Val Phe Ser Glu Asn Ser Asp Gln Val Asn Val Thr Ala Gly Met  
2000 2005 2010

Gln Ala Lys Asn Asp Gly Ile Lys Ile Ile Lys Gly Thr Asn Tyr  
2015 2020 2025

Asn Phe Asn Asp Phe Asn Ser Phe Ile Ser Asn Ile Pro Ala His  
2030 2035 2040

Ser Thr Leu Thr Trp Asn Glu Glu Pro Asn Ser Trp Lys Asn Asn  
2045 2050 2055

Ile Gly Thr Thr Thr Lys Thr Val Thr Val Thr Leu Pro Asn His  
2060 2065 2070

Gln Gly Thr Arg Thr Val Asp Ile Pro Ile Thr Ile Tyr Pro Thr  
2075 2080 2085

Val Thr Ala Lys Asn Pro Val Arg Asp Gln Lys Gly Arg Asn Leu  
2090 2095 2100

Thr Asn Gly Thr Asp Val Tyr Asn Tyr Ile Ile Phe Glu Asn Asn  
2105 2110 2115

Asn Arg Leu Gly Gly Thr Ala Ser Trp Lys Asp Asn Arg Gln Pro  
2120 2125 2130

Asp Lys Asn Ile Ala Gly Val Gln Asn Leu Ile Ala Leu Val Asn  
2135 2140 2145

Tyr Pro Gly Ile Ser Thr Pro Leu Glu Val Pro Val Lys Val Trp  
2150 2155 2160

Val Tyr Asn Phe Asp Phe Thr Gln Pro Ile Tyr Lys Ile Gln Val  
2165 2170 2175

Gly Asp Thr Phe Pro Lys Gly Thr Trp Ala Gly Tyr Tyr Lys His  
2180 2185 2190

Leu Glu Asn Gly Glu Gly Leu Pro Ile Asp Gly Trp Lys Phe Tyr  
2195 2200 2205

Trp Asn Gln Gln Ser Thr Gly Thr Thr Ser Asp Gln Trp Gln Ser  
2210 2215 2220

Leu Ala Tyr Thr Arg Thr Pro Phe Val Lys Thr Gly Thr Tyr Asp  
2225 2230 2235

Val Val Asn Pro Ser Asn Trp Gly Val Trp Gln Thr Ser Gln Ser  
2240 2245 2250

Ala Lys Phe Ile Val Thr Asn Ala Lys Pro Asn Gln Pro Thr Ile  
2255 2260 2265

Thr Gln Ser Lys Thr Gly Asp Val Thr Val Thr Pro Gly Ala Val  
2270 2275 2280

Arg Asn Ile Leu Ile Ser Gly Thr Asn Asp Tyr Ile Gln Ala Ser  
2285 2290 2295

Ala Asp Lys Ile Val Ile Asn Lys Asn Gly Asn Lys Leu Thr Thr  
2300 2305 2310

Phe Val Lys Asn Asn Asp Gly Arg Trp Thr Val Glu Thr Gly Ser  
2315 2320 2325

Pro Asp Ile Asn Gly Ile Gly Pro Thr Asn Asn Gly Thr Ala Ile  
2330 2335 2340

Ser Leu Ser Arg Leu Ala Val Arg Pro Gly Asp Ser Ile Glu Ala  
2345 2350 2355

Ile Ala Thr Glu Gly Ser Gly Glu Thr Ile Ser Thr Ser Ala Thr  
2360 2365 2370

Ser Glu Ile Tyr Ile Val Lys Ala Pro Gln Pro Glu Gln Val Ala  
2375 2380 2385

Thr His Thr Tyr Asp Asn Gly Thr Phe Asp Ile Leu Pro Asp Asn  
2390 2395 2400

Ser Arg Asn Ser Leu Asn Pro Thr Glu Arg Val Glu Ile Asn Tyr  
2405 2410 2415

Thr Glu Lys Leu Asn Gly Asn Glu Thr Gln Lys Ser Phe Thr Ile

2420

2425

2430

Thr Lys Asn Asn Asn Gly Lys Trp Thr Ile Asn Asn Lys Pro Asn  
2435 2440 2445

Tyr Val Glu Phe Asn Gln Asp Asn Gly Lys Val Val Phe Ser Ala  
2450 2455 2460

Asn Thr Ile Lys Pro Asn Ser Gln Ile Thr Ile Thr Pro Lys Ala  
2465 2470 2475

Gly Gln Gly Asn Thr Glu Asn Thr Asn Pro Thr Val Ile Gln Ala  
2480 2485 2490

Pro Ala Gln His Thr Leu Thr Ile Asn Glu Ile Val Lys Glu Gln  
2495 2500 2505

Gly Gln Asn Val Thr Asn Asp Asp Ile Asn Asn Ala Val Gln Val  
2510 2515 2520

Pro Asn Lys Asn Arg Val Ala Ile Lys Gln Gly Asn Ala Leu Pro  
2525 2530 2535

Thr Asn Leu Ala Gly Gly Ser Thr Ser His Ile Pro Val Val Ile  
2540 2545 2550

Tyr Tyr Ser Asp Gly Ser Ser Glu Glu Ala Thr Glu Thr Val Arg  
2555 2560 2565

Thr Lys Val Asn Lys Thr Glu Leu Ile Asn Ala Arg Arg Arg Leu  
2570 2575 2580

Asp Glu Glu Ile Ser Lys Glu Asn Lys Thr Pro Ser Ser Ile Arg  
2585 2590 2595

Asn Phe Asp Gln Ala Met Asn Arg Ala Gln Ser Gln Ile Asn Thr  
2600 2605 2610

Ala Lys Ser Asp Ala Asp Gln Val Ile Gly Thr Glu Phe Ala Thr  
2615 2620 2625

Pro Gln Gln Val Asn Ser Ala Leu Ser Lys Val Gln Ala Ala Gln  
2630 2635 2640

Asn Lys Ile Asn Glu Ala Lys Ala Leu Leu Gln Asn Lys Ala Asp  
2645 2650 2655

Asn Ser Gln Leu Val Arg Ala Lys Glu Gln Leu Gln Gln Ser Ile  
2660 2665 2670

Gln Pro Ala Ala Ser Thr Asp Gly Met Thr Gln Asp Ser Thr Arg  
2675 2680 2685

Asn Tyr Lys Asn Lys Arg Gln Ala Ala Glu Gln Ala Ile Gln His  
2690 2695 2700

Ala Asn Ser Val Ile Asn Asn Gly Asp Ala Thr Ser Gln Gln Ile  
2705 2710 2715

Asn Asp Ala Lys Asn Thr Val Glu Gln Ala Gln Arg Asp Tyr Val  
2720 2725 2730

Glu Ala Lys Ser Asn Leu Arg Ala Asp Lys Ser Gln Leu Gln Ser  
2735 2740 2745

Ala Tyr Asp Thr Leu Asn Arg Asp Val Leu Thr Asn Asp Lys Lys  
2750 2755 2760

Pro Ala Ser Val Arg Arg Tyr Asn Glu Ala Ile Ser Asn Ile Arg  
2765 2770 2775

Lys Glu Leu Asp Thr Ala Lys Ala Asp Ala Ser Ser Thr Leu Arg  
2780 2785 2790

Asn Thr Asn Pro Ser Val Glu Gln Val Arg Asp Ala Leu Asn Lys  
2795 2800 2805

Ile Asn Thr Val Gln Pro Lys Val Asn Gln Ala Ile Ala Leu Leu  
2810 2815 2820

Gln Pro Lys Glu Asn Asn Ser Glu Leu Val Gln Ala Lys Lys Arg  
2825 2830 2835

Leu Gln Asp Ala Val Asn Asp Ile Pro Gln Thr Gln Gly Met Thr  
2840 2845 2850

Gln Gln Thr Ile Asn Asn Tyr Asn Asp Lys Gln Arg Glu Ala Glu  
2855 2860 2865

Arg Ala Leu Thr Ser Ala Gln Arg Val Ile Asp Asn Gly Asp Ala  
2870 2875 2880

Thr Thr Gln Glu Ile Thr Ser Glu Lys Ser Lys Val Glu Gln Ala  
2885 2890 2895

Met Gln Ala Leu Thr Asn Ala Lys Ser Asn Leu Arg Ala Asp Lys  
2900 2905 2910

Asn Glu Leu Gln Thr Ala Tyr Asn Lys Leu Ile Glu Asn Val Ser  
2915 2920 2925

Thr Asn Gly Lys Lys Pro Ala Ser Ile Arg Gln Tyr Glu Thr Ala  
2930 2935 2940

Lys Ala Arg Ile Gln Asn Gln Ile Asn Asp Ala Lys Asn Glu Ala  
2945 2950 2955

Glu Arg Ile Leu Gly Asn Asp Asn Pro Gln Val Ser Gln Val Thr  
2960 2965 2970

Gln Ala Leu Asn Lys Ile Lys Ala Ile Gln Pro Lys Leu Thr Glu  
2975 2980 2985

Ala Ile Asn Met Leu Gln Asn Lys Glu Asn Asn Thr Glu Leu Val  
2990 2995 3000

Asn Ala Lys Asn Arg Leu Glu Asn Ala Val Asn Asp Thr Asp Pro  
3005 3010 3015

Thr His Gly Met Thr Gln Glu Thr Ile Asn Asn Tyr Asn Ala Lys  
3020 3025 3030

Lys Arg Glu Ala Gln Asn Glu Ile Gln Lys Ala Asn Met Ile Ile  
3035 3040 3045

Asn Asn Gly Asp Ala Thr Ala Gln Asp Ile Ser Ser Glu Lys Ser  
3050 3055 3060

Lys Val Glu Gln Val Leu Gln Ala Leu Gln Asn Ala Lys Asn Asp  
3065 3070 3075

Leu Arg Ala Asp Lys Arg Glu Leu Gln Thr Ala Tyr Asn Lys Leu  
3080 3085 3090

Ile Gln Asn Val Asn Thr Asn Gly Lys Lys Pro Ser Ser Ile Gln  
3095 3100 3105

Asn Tyr Lys Ser Ala Arg Arg Asn Ile Glu Asn Gln Tyr Asn Thr  
3110 3115 3120

Ala Lys Asn Glu Ala His Asn Val Leu Glu Asn Thr Asn Pro Thr  
3125 3130 3135

Val Asn Ala Val Glu Asp Ala Leu Arg Lys Ile Asn Ala Ile Gln  
3140 3145 3150

Pro Glu Val Thr Lys Ala Ile Asn Ile Leu Gln Asp Lys Glu Asp  
3155 3160 3165

Asn Ser Glu Leu Val Arg Ala Lys Glu Lys Leu Asp Gln Ala Ile  
3170 3175 3180

Asn Ser Gln Pro Ser Leu Asn Gly Met Thr Gln Glu Ser Ile Asn  
3185 3190 3195

Asn Tyr Thr Thr Lys Arg Arg Glu Ala Gln Asn Ile Ala Ser Ser  
3200 3205 3210

Ala Asp Thr Ile Ile Asn Asn Gly Asp Ala Ser Ile Glu Gln Ile  
3215 3220 3225

Thr Glu Asn Lys Ile Arg Val Glu Glu Ala Thr Asn Ala Leu Asn  
3230 3235 3240

Glu Ala Lys Gln His Leu Thr Ala Asp Thr Thr Ser Leu Lys Thr  
3245 3250 3255

Glu Val Arg Lys Leu Ser Arg Arg Gly Asp Thr Asn Asn Lys Lys  
3260 3265 3270

Pro Ser Ser Val Ser Ala Tyr Asn Asn Thr Ile His Ser Leu Gln

3275	3280	3285
Ser Glu Ile Thr Gln Thr Glu Asn Arg Ala Asn Thr Ile Ile Asn		
3290	3295	3300
Lys Pro Ile Arg Ser Val Glu Glu Val Asn Asn Ala Leu His Glu		
3305	3310	3315
Val Asn Gln Leu Asn Gln Arg Leu Thr Asp Thr Ile Asn Leu Leu		
3320	3325	3330
Gln Pro Leu Ala Asn Lys Glu Ser Leu Lys Glu Ala Arg Asn Arg		
3335	3340	3345
Leu Glu Ser Lys Ile Asn Glu Thr Val Gln Thr Asp Gly Met Thr		
3350	3355	3360
Gln Gln Ser Val Glu Asn Tyr Lys Gln Ala Lys Ile Lys Ala Gln		
3365	3370	3375
Asn Glu Ser Ser Ile Ala Gln Thr Leu Ile Asn Asn Gly Asp Ala		
3380	3385	3390
Ser Asp Gln Glu Val Ser Thr Glu Ile Glu Lys Leu Asn Gln Lys		
3395	3400	3405
Leu Ser Glu Leu Thr Asn Ser Ile Asn His Leu Thr Val Asn Lys		
3410	3415	3420
Glu Pro Leu Glu Thr Ala Lys Asn Gln Leu Gln Ala Asn Ile Asp		
3425	3430	3435
Gln Lys Pro Ser Thr Asp Gly Met Thr Gln Gln Ser Val Gln Ser		
3440	3445	3450
Tyr Glu Arg Lys Leu Gln Glu Ala Lys Asp Lys Ile Asn Ser Ile		
3455	3460	3465
Asn Asn Val Leu Ala Asn Asn Pro Asp Val Asn Ala Ile Arg Thr		
3470	3475	3480
Asn Lys Val Glu Thr Glu Gln Ile Asn Asn Glu Leu Thr Gln Ala		
3485	3490	3495

Lys Gln Gly Leu Thr Val Asp Lys Gln Pro Leu Ile Asn Ala Lys  
3500 3505 3510

Thr Ala Leu Gln Gln Ser Leu Asp Asn Gln Pro Ser Thr Thr Gly  
3515 3520 3525

Met Thr Glu Ala Thr Ile Gln Asn Tyr Asn Ala Lys Arg Gln Lys  
3530 3535 3540

Ala Glu Gln Val Ile Gln Asn Ala Asn Lys Ile Ile Glu Asn Ala  
3545 3550 3555

Gln Pro Ser Val Gln Gln Val Ser Asp Glu Lys Ser Lys Val Glu  
3560 3565 3570

Gln Ala Leu Ser Glu Leu Asn Asn Ala Lys Ser Ala Leu Arg Ala  
3575 3580 3585

Asp Lys Gln Glu Leu Gln Gln Ala Tyr Asn Gln Leu Ile Gln Pro  
3590 3595 3600

Thr Asp Leu Asn Asn Lys Lys Pro Ala Ser Ile Thr Ala Tyr Asn  
3605 3610 3615

Gln Arg Tyr Gln Gln Phe Ser Asn Glu Leu Asn Ser Thr Lys Thr  
3620 3625 3630

Asn Thr Asp Arg Ile Leu Lys Glu Gln Asn Pro Ser Val Ala Asp  
3635 3640 3645

Val Asn Asn Ala Leu Asn Lys Val Arg Glu Val Gln Gln Lys Leu  
3650 3655 3660

Asn Glu Ala Arg Ala Leu Leu Gln Asn Lys Glu Asp Asn Ser Ala  
3665 3670 3675

Leu Val Arg Ala Lys Glu Gln Leu Gln Gln Ala Val Asp Gln Val  
3680 3685 3690

Pro Ser Thr Glu Gly Met Thr Gln Gln Thr Lys Asp Asp Tyr Asn  
3695 3700 3705

Ser Lys Gln Gln Ala Ala Gln Gln Glu Ile Ser Lys Ala Gln Gln  
3710 3715 3720

Val Ile Asp Asn Gly Asp Ala Thr Thr Gln Gln Ile Ser Asn Ala  
3725 3730 3735

Lys Thr Asn Val Glu Arg Ala Leu Glu Ala Leu Asn Asn Ala Lys  
3740 3745 3750

Thr Gly Leu Arg Ala Asp Lys Glu Glu Leu Gln Asn Ala Tyr Asn  
3755 3760 3765

Gln Leu Thr Gln Asn Ile Asp Thr Ser Gly Lys Thr Pro Ala Ser  
3770 3775 3780

Ile Arg Lys Tyr Asn Glu Ala Lys Ser Arg Ile Gln Thr Gln Ile  
3785 3790 3795

Asp Ser Ala Lys Asn Glu Ala Asn Ser Ile Leu Thr Asn Asp Asn  
3800 3805 3810

Pro Gln Val Ser Gln Val Thr Ala Ala Leu Asn Lys Ile Lys Ala  
3815 3820 3825

Val Gln Pro Glu Leu Asp Lys Ala Ile Ala Met Leu Lys Asn Lys  
3830 3835 3840

Glu Asn Asn Asn Ala Leu Val Gln Ala Lys Gln Gln Leu Gln Gln  
3845 3850 3855

Ile Val Asn Glu Val Asp Pro Thr Gln Gly Met Thr Thr Asp Thr  
3860 3865 3870

Ala Asn Asn Tyr Lys Ser Lys Lys Arg Glu Ala Glu Asp Glu Ile  
3875 3880 3885

Gln Lys Ala Gln Gln Ile Ile Asn Asn Gly Asp Ala Thr Glu Gln  
3890 3895 3900

Gln Ile Thr Asn Glu Thr Asn Arg Val Asn Gln Ala Ile Asn Ala  
3905 3910 3915

Ile Asn Lys Ala Lys Asn Asp Leu Arg Ala Asp Lys Ser Gln Leu  
3920 3925 3930

Glu Asn Ala Tyr Asn Gln Leu Ile Gln Asn Val Asp Thr Asn Gly  
3935 3940 3945

Lys Lys Pro Ala Ser Ile Gln Gln Tyr Gln Ala Ala Arg Gln Ala  
3950 3955 3960

Ile Glu Thr Gln Tyr Asn Asn Ala Lys Ser Glu Ala His Gln Ile  
3965 3970 3975

Leu Glu Asn Ser Asn Pro Ser Val Asn Glu Val Ala Gln Ala Leu  
3980 3985 3990

Gln Lys Val Glu Ala Val Gln Leu Lys Val Asn Asp Ala Ile His  
3995 4000 4005

Ile Leu Gln Asn Lys Glu Asn Asn Ser Ala Leu Val Thr Ala Lys  
4010 4015 4020

Asn Gln Leu Gln Gln Ser Val Asn Asp Gln Pro Leu Thr Thr Gly  
4025 4030 4035

Met Thr Gln Asp Ser Ile Asn Asn Tyr Glu Ala Lys Arg Asn Glu  
4040 4045 4050

Ala Gln Ser Ala Ile Arg Asn Ala Glu Ala Val Ile Asn Asn Gly  
4055 4060 4065

Asp Ala Thr Ala Lys Gln Ile Ser Asp Glu Lys Ser Lys Val Glu  
4070 4075 4080

Gln Ala Leu Ala His Leu Asn Asp Ala Lys Gln Gln Leu Thr Ala  
4085 4090 4095

Asp Thr Thr Glu Leu Gln Thr Ala Val Gln Gln Leu Asn Arg Arg  
4100 4105 4110

Gly Asp Thr Asn Asn Lys Lys Pro Arg Ser Ile Asn Ala Tyr Asn  
4115 4120 4125

Lys Ala Ile Gln Ser Leu Glu Thr Gln Ile Thr Ser Ala Lys Asp

4130	4135	4140
Asn Ala Asn Ala Val Ile Gln Lys Pro Ile Arg Thr Val Gln Glu		
4145	4150	4155
Val Asn Asn Ala Leu Gln Gln Val Asn Gln Leu Asn Gln Gln Leu		
4160	4165	4170
Thr Glu Ala Ile Asn Gln Leu Gln Pro Leu Ser Asn Asn Asp Ala		
4175	4180	4185
Leu Lys Ala Ala Arg Leu Asn Leu Glu Asn Lys Ile Asn Gln Thr		
4190	4195	4200
Val Gln Thr Asp Gly Met Thr Gln Gln Ser Ile Glu Ala Tyr Gln		
4205	4210	4215
Asn Ala Lys Arg Val Ala Gln Asn Glu Ser Asn Thr Ala Leu Ala		
4220	4225	4230
Leu Ile Asn Asn Gly Asp Ala Asp Glu Gln Gln Ile Thr Thr Glu		
4235	4240	4245
Thr Asp Arg Val Asn Gln Gln Thr Thr Asn Leu Thr Gln Ala Ile		
4250	4255	4260
Asn Gly Leu Thr Val Asn Lys Glu Pro Leu Glu Thr Ala Lys Thr		
4265	4270	4275
Ala Leu Gln Asn Asn Ile Asp Gln Val Pro Ser Thr Asp Gly Met		
4280	4285	4290
Thr Gln Gln Ser Val Ala Asn Tyr Asn Gln Lys Leu Gln Ile Ala		
4295	4300	4305
Lys Asn Glu Ile Asn Thr Ile Asn Asn Val Leu Ala Asn Asn Pro		
4310	4315	4320
Asp Val Asn Ala Ile Lys Thr Asn Lys Ala Glu Ala Glu Arg Ile		
4325	4330	4335
Ser Asn Asp Leu Thr Gln Ala Lys Asn Asn Leu Gln Val Asp Thr		
4340	4345	4350

Gln Pro Leu Glu Lys Ile Lys Arg Gln Leu Gln Asp Glu Ile Asp  
4355 4360 4365

Gln Gly Thr Asn Thr Asp Gly Met Thr Gln Asp Ser Val Asp Asn  
4370 4375 4380

Tyr Asn Asp Ser Leu Ser Ala Ala Ile Ile Glu Lys Gly Lys Val  
4385 4390 4395

Asn Lys Leu Leu Lys Arg Asn Pro Thr Val Glu Gln Val Lys Glu  
4400 4405 4410

Ser Val Ala Asn Ala Gln Gln Val Ile Gln Asp Leu Gln Asn Ala  
4415 4420 4425

Arg Thr Ser Leu Val Pro Asp Lys Thr Gln Leu Gln Glu Ala Lys  
4430 4435 4440

Asn Arg Leu Glu Asn Ser Ile Asn Gln Gln Thr Asp Thr Asp Gly  
4445 4450 4455

Met Thr Gln Asp Ser Leu Asn Asn Tyr Asn Asp Lys Leu Ala Lys  
4460 4465 4470

Ala Arg Gln Asn Leu Glu Lys Ile Ser Lys Val Leu Gly Gly Gln  
4475 4480 4485

Pro Thr Val Ala Glu Ile Arg Gln Asn Thr Asp Glu Ala Asn Ala  
4490 4495 4500

His Lys Gln Ala Leu Asp Thr Ala Arg Ser Gln Leu Thr Leu Asn  
4505 4510 4515

Arg Glu Pro Tyr Ile Asn His Ile Asn Asn Glu Ser His Leu Asn  
4520 4525 4530

Asn Ala Gln Lys Asp Asn Phe Lys Ala Gln Val Asn Ser Ala Pro  
4535 4540 4545

Asn His Asn Thr Leu Glu Thr Ile Lys Asn Lys Ala Asp Thr Leu  
4550 4555 4560

Asn Gln Ser Met Thr Ala Leu Ser Glu Ser Ile Ala Asp Tyr Glu  
4565 4570 4575

Asn Gln Lys Gln Gln Glu Asn Tyr Leu Asp Ala Ser Asn Asn Lys  
4580 4585 4590

Arg Gln Asp Tyr Asp Asn Ala Val Asn Ala Ala Lys Gly Ile Leu  
4595 4600 4605

Asn Gln Thr Gln Ser Pro Thr Met Ser Ala Asp Val Ile Asp Gln  
4610 4615 4620

Lys Ala Glu Asp Val Lys Arg Thr Lys Thr Ala Leu Asp Gly Asn  
4625 4630 4635

Gln Arg Leu Glu Val Ala Lys Gln Gln Ala Leu Asn His Leu Asn  
4640 4645 4650

Thr Leu Asn Asp Leu Asn Asp Ala Gln Arg Gln Thr Leu Thr Asp  
4655 4660 4665

Thr Ile Asn His Ser Pro Asn Ile Asn Ser Val Asn Gln Ala Lys  
4670 4675 4680

Glu Lys Ala Asn Thr Val Asn Thr Ala Met Thr Gln Leu Lys Gln  
4685 4690 4695

Thr Ile Ala Asn Tyr Asp Asp Glu Leu His Asp Gly Asn Tyr Ile  
4700 4705 4710

Asn Ala Asp Lys Asp Lys Lys Asp Ala Tyr Asn Asn Ala Val Asn  
4715 4720 4725

Asn Ala Lys Gln Leu Ile Asn Gln Ser Asp Ala Asn Gln Ala Gln  
4730 4735 4740

Leu Asp Pro Ala Glu Ile Asn Lys Val Thr Gln Arg Val Asn Thr  
4745 4750 4755

Thr Lys Asn Asp Leu Asn Gly Asn Asp Lys Leu Ala Glu Ala Lys  
4760 4765 4770

Arg Asp Ala Asn Thr Thr Ile Asp Gly Leu Thr Tyr Leu Asn Glu  
4775 4780 4785

Ala Gln Arg Asn Lys Ala Lys Glu Asn Val Gly Lys Ala Ser Thr  
4790 4795 4800

Lys Thr Asn Ile Thr Ser Gln Leu Gln Asp Tyr Asn Gln Leu Asn  
4805 4810 4815

Ile Ala Met Gln Ala Leu Arg Asn Ser Val Asn Asp Val Asn Asn  
4820 4825 4830

Val Lys Ala Asn Ser Asn Tyr Ile Asn Glu Asp Asn Gly Pro Lys  
4835 4840 4845

Glu Ala Tyr Asn Gln Ala Val Thr His Ala Gln Thr Leu Ile Asn  
4850 4855 4860

Ala Gln Ser Asn Pro Glu Met Ser Arg Asp Val Val Asn Gln Lys  
4865 4870 4875

Thr Gln Ala Val Asn Thr Ala His Gln Asn Leu His Gly Gln Gln  
4880 4885 4890

Lys Leu Glu Gln Ala Gln Ser Ser Ala Asn Thr Glu Ile Gly Asn  
4895 4900 4905

Leu Pro Asn Leu Thr Asn Thr Gln Lys Ala Lys Glu Lys Glu Leu  
4910 4915 4920

Val Asn Ser Lys Gln Thr Arg Thr Glu Val Gln Glu Gln Leu Asn  
4925 4930 4935

Gln Ala Lys Ser Leu Asp Ser Ser Met Gly Thr Leu Lys Ser Leu  
4940 4945 4950

Val Ala Lys Gln Pro Thr Val Gln Lys Thr Ser Val Tyr Ile Asn  
4955 4960 4965

Glu Asp Gln Pro Glu Gln Ser Ala Tyr Asn Asp Ser Ile Thr Met  
4970 4975 4980

Gly Gln Thr Ile Ile Asn Lys Thr Ala Asp Pro Val Leu Asp Lys

4985

4990

4995

Thr Leu Val Asp Asn Ala Ile Ser Asn Ile Ser Thr Lys Glu Asn  
5000 5005 5010

Ala Leu His Gly Glu Gln Lys Leu Thr Thr Ala Lys Thr Glu Ala  
5015 5020 5025

Ile Asn Ala Leu Asn Thr Leu Ala Asp Leu Asn Thr Pro Gln Lys  
5030 5035 5040

Glu Ala Ile Lys Thr Ala Ile Asn Thr Ala His Thr Arg Thr Asp  
5045 5050 5055

Val Thr Ala Glu Gln Ser Lys Ala Asn Gln Ile Asn Ser Ala Met  
5060 5065 5070

His Thr Leu Arg Gln Asn Ile Ser Asp Asn Glu Ser Val Thr Asn  
5075 5080 5085

Glu Ser Asn Tyr Ile Asn Ala Glu Pro Glu Lys Gln His Ala Phe  
5090 5095 5100

Thr Glu Ala Leu Asn Asn Ala Lys Glu Ile Val Asn Glu Gln Gln  
5105 5110 5115

Ala Thr Leu Asp Ala Asn Ser Ile Asn Gln Lys Ala Gln Ala Ile  
5120 5125 5130

Leu Thr Thr Lys Asn Ala Leu Asp Gly Glu Glu Gln Leu Arg Arg  
5135 5140 5145

Ala Lys Glu Asn Ala Asp Gln Glu Ile Asn Thr Leu Asn Gln Leu  
5150 5155 5160

Thr Asp Ala Gln Arg Asn Ser Glu Lys Gly Leu Val Asn Ser Ser  
5165 5170 5175

Gln Thr Arg Thr Glu Val Ala Ser Gln Leu Ala Lys Ala Lys Glu  
5180 5185 5190

Leu Asn Lys Val Met Glu Gln Leu Asn His Leu Ile Asn Gly Lys  
5195 5200 5205

Asn Gln Met Ile Asn Ser Ser Lys Phe Ile Asn Glu Asp Ala Asn  
5210 5215 5220

Gln Gln Gln Ala Tyr Ser Asn Ala Ile Ala Ser Ala Glu Ala Leu  
5225 5230 5235

Lys Asn Lys Ser Gln Asn Pro Glu Leu Asp Lys Val Thr Ile Glu  
5240 5245 5250

Gln Ala Ile Asn Asn Ile Asn Ser Ala Ile Asn Asn Leu Asn Gly  
5255 5260 5265

Glu Ala Lys Leu Thr Lys Ala Lys Glu Asp Ala Val Ala Ser Ile  
5270 5275 5280

Asn Asn Leu Ser Gly Leu Thr Asn Glu Gln Lys Pro Lys Glu Asn  
5285 5290 5295

Gln Ala Val Asn Gly Ala Gln Thr Arg Asp Gln Val Ala Asn Lys  
5300 5305 5310

Leu Arg Asp Ala Glu Ala Leu Asp Gln Ser Met Gln Thr Leu Arg  
5315 5320 5325

Asp Leu Val Asn Asn Gln Asn Ala Ile His Ser Thr Ser Asn Tyr  
5330 5335 5340

Phe Asn Glu Asp Ser Thr Gln Lys Asn Thr Tyr Asp Asn Ala Ile  
5345 5350 5355

Asp Asn Gly Ser Thr Tyr Ile Thr Gly Gln His Asn Pro Glu Leu  
5360 5365 5370

Asn Lys Ser Thr Ile Asp Gln Thr Ile Ser Arg Ile Asn Thr Ala  
5375 5380 5385

Lys Asn Asp Leu His Gly Val Glu Lys Leu Gln Arg Asp Lys Gly  
5390 5395 5400

Thr Ala Asn Gln Glu Ile Gly Gln Leu Gly Tyr Leu Asn Asp Pro  
5405 5410 5415

Gln Lys Ser Gly Glu Glu Ser Leu Val Asn Gly Ser Asn Thr Arg  
5420 5425 5430

Ser Glu Val Glu Glu His Leu Asn Glu Ala Lys Ser Leu Asn Asn  
5435 5440 5445

Ala Met Lys Gln Leu Arg Asp Lys Val Ala Glu Lys Thr Asn Val  
5450 5455 5460

Lys Gln Ser Ser Asp Tyr Ile Asn Asp Ser Thr Glu His Gln Arg  
5465 5470 5475

Gly Tyr Asp Gln Ala Leu Gln Glu Ala Glu Asn Ile Ile Asn Glu  
5480 5485 5490

Ile Gly Asn Pro Thr Leu Asn Lys Ser Glu Ile Glu Gln Lys Leu  
5495 5500 5505

Gln Gln Leu Thr Asp Ala Gln Asn Ala Leu Gln Gly Ser His Leu  
5510 5515 5520

Leu Glu Glu Ala Lys Asn Asn Ala Ile Thr Gly Ile Asn Lys Leu  
5525 5530 5535

Thr Ala Leu Asn Asp Ala Gln Arg Gln Lys Ala Ile Glu Asn Val  
5540 5545 5550

Gln Ala Gln Gln Thr Ile Pro Ala Val Asn Gln Gln Leu Thr Leu  
5555 5560 5565

Asp Arg Glu Ile Asn Thr Ala Met Gln Ala Leu Arg Asp Lys Val  
5570 5575 5580

Gly Gln Gln Asn Asn Val His Gln Gln Ser Asn Tyr Phe Asn Glu  
5585 5590 5595

Asp Glu Gln Pro Lys His Asn Tyr Asp Asn Ser Val Gln Ala Gly  
5600 5605 5610

Gln Thr Ile Ile Asp Lys Leu Gln Asp Pro Ile Met Asn Lys Asn  
5615 5620 5625

Glu Ile Glu Gln Ala Ile Asn Gln Ile Asn Thr Thr Gln Thr Ala  
5630 5635 5640

Leu Ser Gly Glu Asn Lys Leu His Thr Asp Gln Glu Ser Thr Asn  
5645 5650 5655

Arg Gln Ile Glu Gly Leu Ser Ser Leu Asn Thr Ala Gln Ile Asn  
5660 5665 5670

Ala Glu Lys Asp Leu Val Asn Gln Ala Lys Thr Arg Thr Asp Val  
5675 5680 5685

Ala Gln Lys Leu Ala Ala Ala Lys Glu Ile Asn Ser Ala Met Ser  
5690 5695 5700

Asn Leu Arg Asp Gly Ile Gln Asn Lys Glu Asp Ile Lys Arg Ser  
5705 5710 5715

Ser Ala Tyr Ile Asn Ala Asp Pro Thr Lys Val Thr Ala Tyr Asp  
5720 5725 5730

Gln Ala Leu Gln Asn Ala Glu Asn Ile Ile Asn Ala Thr Pro Asn  
5735 5740 5745

Val Glu Leu Asn Lys Ala Thr Ile Glu Gln Ala Leu Ser Arg Val  
5750 5755 5760

Gln Gln Ala Gln Gln Asp Leu Asp Gly Val Gln Gln Leu Ala Asn  
5765 5770 5775

Ala Lys Gln Gln Ala Thr Gln Thr Val Asn Gly Leu Asn Ser Leu  
5780 5785 5790

Asn Asp Gly Gln Lys Arg Glu Leu Asn Leu Leu Ile Asn Ser Ala  
5795 5800 5805

Asn Thr Arg Thr Lys Val Gln Glu Glu Leu Asn Lys Ala Thr Glu  
5810 5815 5820

Leu Asn His Ala Met Glu Ala Leu Arg Asn Ser Val Gln Asn Val  
5825 5830 5835

Asp Gln Val Lys Gln Ser Ser Asn Tyr Val Asn Glu Asp Gln Pro

5840 5845 5850

Glu Gln His Asn Tyr Asp Asn Ala Val Asn Glu Ala Gln Ala Thr  
5855 5860 5865

Ile Asn Asn Asn Ala Gln Pro Val Leu Asp Lys Leu Ala Ile Glu  
5870 5875 5880

Arg Leu Thr Gln Thr Val Asn Thr Thr Lys Asp Ala Leu His Gly  
5885 5890 5895

Ala Gln Lys Leu Thr Gln Asp Gln Gln Ala Ala Glu Thr Gly Ile  
5900 5905 5910

Arg Gly Leu Thr Ser Leu Asn Glu Pro Gln Lys Asn Ala Glu Val  
5915 5920 5925

Ala Lys Val Thr Ala Ala Thr Thr Arg Asp Glu Val Arg Asn Ile  
5930 5935 5940

Arg Gln Glu Ala Thr Thr Leu Asp Thr Ala Met Leu Gly Leu Arg  
5945 5950 5955

Lys Ser Ile Lys Asp Lys Asn Asp Thr Lys Asn Ser Ser Lys Tyr  
5960 5965 5970

Ile Asn Glu Asp His Asp Gln Gln Gln Ala Tyr Asp Asn Ala Val  
5975 5980 5985

Asn Asn Ala Gln Gln Val Ile Asp Glu Thr Gln Ala Thr Leu Ser  
5990 5995 6000

Ser Asp Thr Ile Asn Gln Leu Ala Asn Ala Val Thr Gln Ala Lys  
6005 6010 6015

Ser Asn Leu His Gly Asp Thr Lys Leu Gln His Asp Lys Asp Ser  
6020 6025 6030

Ala Lys Gln Thr Ile Ala Gln Leu Gln Asn Leu Asn Ser Ala Gln  
6035 6040 6045

Lys His Met Glu Asp Ser Leu Ile Asp Asn Glu Ser Thr Arg Thr  
6050 6055 6060

Gln Val Gln His Asp Leu Thr Glu Ala Gln Ala Leu Asp Gly Leu  
6065 6070 6075

Met Gly Ala Leu Lys Glu Ser Ile Lys Asp Tyr Thr Asn Ile Val  
6080 6085 6090

Ser Asn Gly Asn Tyr Ile Asn Ala Glu Pro Ser Lys Lys Gln Ala  
6095 6100 6105

Tyr Asp Ala Ala Val Gln Asn Ala Gln Asn Ile Ile Asn Gly Thr  
6110 6115 6120

Asn Gln Pro Thr Ile Asn Lys Gly Asn Val Thr Thr Ala Thr Gln  
6125 6130 6135

Thr Val Lys Asn Thr Lys Asp Ala Leu Asp Gly Asp His Arg Leu  
6140 6145 6150

Glu Glu Ala Lys Asn Asn Ala Asn Gln Thr Ile Arg Asn Leu Ser  
6155 6160 6165

Asn Leu Asn Asn Ala Gln Lys Asp Ala Glu Lys Asn Leu Val Asn  
6170 6175 6180

Ser Ala Ser Thr Leu Glu Gln Val Gln Gln Asn Leu Gln Thr Ala  
6185 6190 6195

Gln Gln Leu Asp Asn Ala Met Gly Glu Leu Arg Gln Ser Ile Ala  
6200 6205 6210

Lys Lys Asp Gln Val Lys Ala Asp Ser Lys Tyr Leu Asn Glu Asp  
6215 6220 6225

Pro Gln Ile Lys Gln Asn Tyr Asp Asp Ala Val Gln Arg Val Glu  
6230 6235 6240

Thr Ile Ile Asn Glu Thr Gln Asn Pro Glu Leu Leu Lys Ala Asn  
6245 6250 6255

Ile Asp Gln Ala Thr Gln Ser Val Gln Asn Ala Glu Gln Ala Leu  
6260 6265 6270

His Gly Ala Glu Lys Leu Asn Gln Asp Lys Gln Thr Ser Ser Thr  
6275 6280 6285

Glu Leu Asp Gly Leu Thr Asp Leu Thr Asp Ala Gln Arg Glu Lys  
6290 6295 6300

Leu Arg Glu Gln Ile Asn Thr Ser Asn Ser Arg Asp Asp Ile Lys  
6305 6310 6315

Gln Lys Ile Glu Gln Ala Lys Ala Leu Asn Asp Ala Met Lys Lys  
6320 6325 6330

Leu Lys Glu Gln Val Ala Gln Lys Asp Gly Val His Ala Asn Ser  
6335 6340 6345

Asp Tyr Thr Asn Glu Asp Ser Ala Gln Lys Asp Ala Tyr Asn Asn  
6350 6355 6360

Ala Leu Lys Gln Ala Glu Asp Ile Ile Asn Asn Ser Ser Asn Pro  
6365 6370 6375

Asn Leu Asn Ala Gln Asp Ile Thr Asn Ala Leu Asn Asn Ile Lys  
6380 6385 6390

Gln Ala Gln Asp Asn Leu His Gly Ala Gln Lys Leu Gln Gln Asp  
6395 6400 6405

Lys Asn Thr Thr Asn Gln Ala Ile Gly Asn Leu Asn His Leu Asn  
6410 6415 6420

Gln Pro Gln Lys Asp Ala Leu Ile Gln Ala Ile Asn Gly Ala Thr  
6425 6430 6435

Ser Arg Asp Gln Val Ala Glu Lys Leu Lys Glu Ala Glu Ala Leu  
6440 6445 6450

Asp Glu Ala Met Lys Gln Leu Glu Asp Gln Val Asn Gln Asp Asp  
6455 6460 6465

Gln Ile Ser Asn Ser Ser Pro Phe Ile Asn Glu Asp Ser Asp Lys  
6470 6475 6480

Gln Lys Thr Tyr Asn Asp Lys Ile Gln Ala Ala Lys Glu Ile Ile  
6485 6490 6495

Asn Gln Thr Ser Asn Pro Thr Leu Asp Lys Gln Lys Ile Ala Asp  
6500 6505 6510

Thr Leu Gln Asn Ile Lys Asp Ala Val Asn Asn Leu His Gly Asp  
6515 6520 6525

Gln Lys Leu Ala Gln Ser Lys Gln Asp Ala Asn Asn Gln Leu Asn  
6530 6535 6540

His Leu Asp Asp Leu Thr Glu Glu Gln Lys Asn His Phe Lys Pro  
6545 6550 6555

Leu Ile Asn Asn Ala Asp Thr Arg Asp Glu Val Asn Lys Gln Leu  
6560 6565 6570

Glu Ile Ala Lys Gln Leu Asn Gly Asp Met Ser Thr Leu His Lys  
6575 6580 6585

Val Ile Asn Asp Lys Asp Gln Ile Gln His Leu Ser Asn Tyr Ile  
6590 6595 6600

Asn Ala Asp Asn Asp Lys Lys Gln Asn Tyr Asp Asn Ala Ile Lys  
6605 6610 6615

Glu Ala Glu Asp Leu Ile His Asn His Pro Asp Thr Leu Asp His  
6620 6625 6630

Lys Ala Leu Gln Asp Leu Leu Asn Lys Ile Asp Gln Ala His Asn  
6635 6640 6645

Glu Leu Asn Gly Glu Ser Arg Phe Lys Gln Ala Leu Asp Asn Ala  
6650 6655 6660

Leu Asn Asp Ile Asp Ser Leu Asn Ser Leu Asn Val Pro Gln Arg  
6665 6670 6675

Gln Thr Val Lys Asp Asn Ile Asn His Val Thr Thr Leu Glu Ser  
6680 6685 6690

Leu Ala Gln Glu Leu Gln Lys Ala Lys Glu Leu Asn Asp Ala Met

6695 6700 6705

Lys Ala Met Arg Asp Ser Ile Met Asn Gln Glu Gln Ile Arg Lys  
6710 6715 6720

Asn Ser Asn Tyr Thr Asn Glu Asp Leu Ala Gln Gln Asn Ala Tyr  
6725 6730 6735

Asn His Ala Val Asp Lys Ile Asn Asn Ile Ile Gly Glu Asp Asn  
6740 6745 6750

Ala Thr Met Asp Pro Gln Ile Ile Lys Gln Ala Thr Gln Asp Ile  
6755 6760 6765

Asn Thr Ala Ile Asn Gly Leu Asn Gly Asp Gln Lys Leu Gln Asp  
6770 6775 6780

Ala Lys Thr Asp Ala Lys Gln Gln Ile Thr Asn Phe Thr Gly Leu  
6785 6790 6795

Thr Glu Pro Gln Lys Gln Ala Leu Glu Asn Ile Ile Asn Gln Gln  
6800 6805 6810

Thr Ser Arg Ala Asn Val Ala Lys Gln Leu Ser His Ala Lys Phe  
6815 6820 6825

Leu Asn Gly Lys Met Glu Glu Leu Lys Val Ala Val Ala Lys Ala  
6830 6835 6840

Ser Leu Val Arg Gln Asn Ser Asn Tyr Ile Asn Glu Asp Val Ser  
6845 6850 6855

Glu Lys Glu Ala Tyr Glu Gln Ala Ile Ala Lys Gly Gln Glu Ile  
6860 6865 6870

Ile Asn Ser Glu Asn Asn Pro Thr Ile Ser Ser Thr Asp Ile Asn  
6875 6880 6885

Arg Thr Ile Gln Glu Ile Asn Asp Ala Glu Gln Asn Leu His Gly  
6890 6895 6900

Asp Asn Lys Leu Arg Gln Ala Gln Glu Ile Ala Lys Asn Glu Ile  
6905 6910 6915

Gln Asn Leu Asp Gly Leu Asn Ser Ala Gln Ile Thr Lys Leu Ile  
6920 6925 6930

Gln Asp Ile Gly Arg Thr Thr Thr Lys Pro Ala Val Thr Gln Lys  
6935 6940 6945

Leu Glu Glu Ala Lys Ala Ile Asn Gln Ala Met Gln Gln Leu Lys  
6950 6955 6960

Gln Ser Ile Ala Asp Lys Asp Ala Thr Leu Asn Ser Ser Asn Tyr  
6965 6970 6975

Leu Asn Glu Asp Ser Glu Lys Lys Leu Ala Tyr Asp Asn Ala Val  
6980 6985 6990

Ser Gln Ala Glu Gln Leu Ile Asn Gln Leu Asn Asp Pro Thr Met  
6995 7000 7005

Asp Ile Ser Asn Ile Gln Ala Ile Thr Gln Lys Val Ile Gln Ala  
7010 7015 7020

Lys Asp Ser Leu His Gly Ala Asn Lys Leu Ala Gln Asn Gln Ala  
7025 7030 7035

Asp Ser Asn Leu Ile Ile Asn Gln Ser Thr Asn Leu Asn Asp Lys  
7040 7045 7050

Gln Lys Gln Ala Leu Asn Asp Leu Ile Asn His Ala Gln Thr Lys  
7055 7060 7065

Gln Gln Val Ala Glu Ile Ile Ala Gln Ala Asn Lys Leu Asn Asn  
7070 7075 7080

Glu Met Gly Thr Leu Lys Thr Leu Val Glu Glu Gln Ser Asn Val  
7085 7090 7095

His Gln Gln Ser Lys Tyr Ile Asn Glu Asp Pro Gln Val Gln Asn  
7100 7105 7110

Ile Tyr Asn Asp Ser Ile Gln Lys Gly Arg Glu Ile Leu Asn Gly  
7115 7120 7125

Thr Thr Asp Asp Val Leu Asn Asn Asn Lys Ile Ala Asp Ala Ile  
7130 7135 7140

Gln Asn Ile His Leu Thr Lys Asn Asp Leu His Gly Asp Gln Lys  
7145 7150 7155

Leu Gln Lys Ala Gln Gln Asp Ala Thr Asn Glu Leu Asn Tyr Leu  
7160 7165 7170

Thr Asn Leu Asn Asn Ser Gln Arg Gln Ser Glu His Asp Glu Ile  
7175 7180 7185

Asn Ser Ala Pro Ser Arg Thr Glu Val Ser Asn Asp Leu Asn His  
7190 7195 7200

Ala Lys Ala Leu Asn Glu Ala Met Arg Gln Leu Glu Asn Glu Val  
7205 7210 7215

Ala Leu Glu Asn Ser Val Lys Lys Leu Ser Asp Phe Ile Asn Glu  
7220 7225 7230

Asp Glu Ala Ala Gln Asn Glu Tyr Ser Asn Ala Leu Gln Lys Ala  
7235 7240 7245

Lys Asp Ile Ile Asn Gly Val Pro Ser Ser Thr Leu Asp Lys Ala  
7250 7255 7260

Thr Ile Glu Asp Ala Leu Leu Glu Leu Gln Asn Ala Arg Glu Ser  
7265 7270 7275

Leu His Gly Glu Gln Lys Leu Gln Glu Ala Lys Asn Gln Ala Val  
7280 7285 7290

Ala Glu Ile Asp Asn Leu Gln Ala Leu Asn Pro Gly Gln Val Leu  
7295 7300 7305

Ala Glu Lys Thr Leu Val Asn Gln Ala Ser Thr Lys Pro Glu Val  
7310 7315 7320

Gln Glu Ala Leu Gln Lys Ala Lys Glu Leu Asn Glu Ala Met Lys  
7325 7330 7335

Ala Leu Lys Thr Glu Ile Asn Lys Lys Glu Gln Ile Lys Ala Asp  
7340 7345 7350

Ser Arg Tyr Val Asn Ala Asp Ser Gly Leu Gln Ala Asn Tyr Asn  
7355 7360 7365

Ser Ala Leu Asn Tyr Gly Ser Gln Ile Ile Ala Thr Thr Gln Pro  
7370 7375 7380

Pro Glu Leu Asn Lys Asp Val Ile Asn Arg Ala Thr Gln Thr Ile  
7385 7390 7395

Lys Thr Ala Glu Asn Asn Leu Asn Gly Gln Ser Lys Leu Ala Glu  
7400 7405 7410

Ala Lys Ser Asp Gly Asn Gln Ser Ile Glu His Leu Gln Gly Leu  
7415 7420 7425

Thr Gln Ser Gln Lys Asp Lys Gln His Asp Leu Ile Asn Gln Ala  
7430 7435 7440

Gln Thr Lys Gln Gln Val Asp Asp Ile Val Asn Asn Ser Lys Gln  
7445 7450 7455

Leu Asp Asn Ser Met Asn Gln Leu Gln Gln Ile Val Asn Asn Asp  
7460 7465 7470

Asn Thr Val Lys Gln Asn Ser Asp Phe Ile Asn Glu Asp Ser Ser  
7475 7480 7485

Gln Gln Asp Ala Tyr Asn His Ala Ile Gln Ala Ala Lys Asp Leu  
7490 7495 7500

Ile Thr Ala His Pro Thr Ile Met Asp Lys Asn Gln Ile Asp Gln  
7505 7510 7515

Ala Ile Glu Asn Ile Lys Gln Ala Leu Asn Asp Leu His Gly Ser  
7520 7525 7530

Asn Lys Leu Ser Glu Asp Lys Lys Glu Ala Ser Glu Gln Leu Gln  
7535 7540 7545

Asn Leu Asn Ser Leu Thr Asn Gly Gln Lys Asp Thr Ile Leu Asn

7550

7555

7560

His Ile Phe Ser Ala Pro Thr Arg Ser Gln Val Gly Glu Lys Ile  
7565 7570 7575

Ala Ser Ala Lys Gln Leu Asn Asn Thr Met Lys Ala Leu Arg Asp  
7580 7585 7590

Ser Ile Ala Asp Asn Asn Glu Ile Leu Gln Ser Ser Lys Tyr Phe  
7595 7600 7605

Asn Glu Asp Ser Gln Gln Asn Ala Tyr Asn Gln Ala Val Asn  
7610 7615 7620

Lys Ala Lys Asn Ile Ile Asn Asp Gln Pro Thr Pro Val Met Ala  
7625 7630 7635

Asn Asp Glu Ile Gln Ser Val Leu Asn Glu Val Lys Gln Thr Lys  
7640 7645 7650

Asp Asn Leu His Gly Asp Gln Lys Leu Ala Asn Asp Lys Thr Asp  
7655 7660 7665

Ala Gln Ala Thr Leu Asn Ala Leu Asn Tyr Leu Asn Gln Ala Gln  
7670 7675 7680

Arg Gly Asn Leu Glu Thr Lys Val Gln Asn Ser Asn Ser Arg Pro  
7685 7690 7695

Glu Val Gln Lys Val Val Gln Leu Ala Asn Gln Leu Asn Asp Ala  
7700 7705 7710

Met Lys Lys Leu Asp Asp Ala Leu Thr Gly Asn Asp Ala Ile Lys  
7715 7720 7725

Gln Thr Ser Asn Tyr Ile Asn Glu Asp Thr Ser Gln Gln Val Asn  
7730 7735 7740

Phe Asp Glu Tyr Thr Asp Arg Gly Lys Asn Ile Val Ala Glu Gln  
7745 7750 7755

Thr Asn Pro Asn Met Ser Pro Thr Asn Ile Asn Thr Ile Ala Asp  
7760 7765 7770

Lys Ile Thr Glu Ala Lys Asn Asp Leu His Gly Val Gln Lys Leu  
7775 7780 7785

Lys Gln Ala Gln Gln Ser Ile Asn Thr Ile Asn Gln Met Thr  
7790 7795 7800

Gly Leu Asn Gln Ala Gln Lys Glu Gln Leu Asn Gln Glu Ile Gln  
7805 7810 7815

Gln Thr Gln Thr Arg Ser Glu Val His Gln Val Ile Asn Lys Ala  
7820 7825 7830

Gln Ala Leu Asn Asp Ser Met Asn Thr Leu Arg Gln Ser Ile Thr  
7835 7840 7845

Asp Glu His Glu Val Lys Gln Thr Ser Asn Tyr Ile Asn Glu Thr  
7850 7855 7860

Val Gly Asn Gln Thr Ala Tyr Asn Asn Ala Val Asp Arg Val Lys  
7865 7870 7875

Gln Ile Ile Asn Gln Thr Ser Asn Pro Thr Met Asn Pro Leu Glu  
7880 7885 7890

Val Glu Arg Ala Thr Ser Asn Val Lys Ile Ser Lys Asp Ala Leu  
7895 7900 7905

His Gly Glu Arg Glu Leu Asn Asp Asn Lys Asn Ser Lys Thr Phe  
7910 7915 7920

Ala Val Asn His Leu Asp Asn Leu Asn Gln Ala Gln Lys Glu Ala  
7925 7930 7935

Leu Thr His Glu Ile Glu Gln Ala Thr Ile Val Ser Gln Val Asn  
7940 7945 7950

Asn Ile Tyr Asn Lys Ala Lys Ala Leu Asn Asn Asp Met Lys Lys  
7955 7960 7965

Leu Lys Asp Ile Val Ala Gln Gln Asp Asn Val Arg Gln Ser Asn  
7970 7975 7980

Asn Tyr Ile Asn Glu Asp Ser Thr Pro Gln Asn Met Tyr Asn Asp  
7985 7990 7995

Thr Ile Asn His Ala Gln Ser Ile Ile Asp Gln Val Ala Asn Pro  
8000 8005 8010

Thr Met Ser His Asp Glu Ile Glu Asn Ala Ile Asn Asn Ile Lys  
8015 8020 8025

His Ala Ile Asn Ala Leu Asp Gly Glu His Lys Leu Gln Gln Ala  
8030 8035 8040

Lys Glu Asn Ala Asn Leu Leu Ile Asn Ser Leu Asn Asp Leu Asn  
8045 8050 8055

Ala Pro Gln Arg Asp Ala Ile Asn Arg Leu Val Asn Glu Ala Gln  
8060 8065 8070

Thr Arg Glu Lys Val Ala Glu Gln Leu Gln Ser Ala Gln Ala Leu  
8075 8080 8085

Asn Asp Ala Met Lys His Leu Arg Asn Ser Ile Gln Asn Gln Ser  
8090 8095 8100

Ser Val Arg Gln Glu Ser Lys Tyr Ile Asn Ala Ser Asp Ala Lys  
8105 8110 8115

Lys Glu Gln Tyr Asn His Ala Val Arg Glu Val Glu Asn Ile Ile  
8120 8125 8130

Asn Glu Gln His Pro Thr Leu Asp Lys Glu Ile Ile Lys Gln Leu  
8135 8140 8145

Thr Asp Gly Val Asn Gln Ala Asn Asn Asp Leu Asn Gly Val Glu  
8150 8155 8160

Leu Leu Asp Ala Asp Lys Gln Asn Ala His Gln Ser Ile Pro Thr  
8165 8170 8175

Leu Met His Leu Asn Gln Ala Gln Gln Asn Ala Leu Asn Glu Lys  
8180 8185 8190

Ile Asn Asn Ala Val Thr Arg Thr Glu Val Ala Ala Ile Ile Gly  
8195 8200 8205

Gln Ala Lys Leu Leu Asp His Ala Met Glu Asn Leu Glu Glu Ser  
8210 8215 8220

Ile Lys Asp Lys Glu Gln Val Lys Gln Ser Ser Asn Tyr Ile Asn  
8225 8230 8235

Glu Asp Ser Asp Val Gln Glu Thr Tyr Asp Asn Ala Val Asp His  
8240 8245 8250

Val Thr Glu Ile Leu Asn Gln Thr Val Asn Pro Thr Leu Ser Ile  
8255 8260 8265

Glu Asp Ile Glu His Ala Ile Asn Glu Val Asn Gln Ala Lys Lys  
8270 8275 8280

Gln Leu Arg Gly Lys Gln Lys Leu Tyr Gln Thr Ile Asp Leu Ala  
8285 8290 8295

Asp Lys Glu Leu Ser Lys Leu Asp Asp Leu Thr Ser Gln Gln Ser  
8300 8305 8310

Ser Ser Ile Ser Asn Gln Ile Tyr Thr Ala Lys Thr Arg Thr Glu  
8315 8320 8325

Val Ala Gln Ala Ile Glu Lys Ala Lys Ser Leu Asn His Ala Met  
8330 8335 8340

Lys Ala Leu Asn Lys Val Tyr Lys Asn Ala Asp Lys Val Leu Asp  
8345 8350 8355

Ser Ser Arg Phe Ile Asn Glu Asp Gln Pro Glu Lys Lys Ala Tyr  
8360 8365 8370

Gln Gln Ala Ile Asn His Val Asp Ser Ile Ile His Arg Gln Thr  
8375 8380 8385

Asn Pro Glu Met Asp Pro Thr Val Ile Asn Ser Ile Thr His Glu  
8390 8395 8400

Leu Glu Thr Ala Gln Asn Asn Leu His Gly Asp Gln Lys Leu Ala

8405

8410

8415

His Ala Gln Gln Asp Ala Ala Asn Val Ile Asn Gly Leu Ile His  
8420 8425 8430

Leu Asn Val Ala Gln Arg Glu Val Met Ile Asn Thr Asn Thr Asn  
8435 8440 8445

Ala Thr Thr Arg Glu Lys Val Ala Lys Asn Leu Asp Asn Ala Gln  
8450 8455 8460

Ala Leu Asp Lys Ala Met Glu Thr Leu Gln Gln Val Val Ala His  
8465 8470 8475

Lys Asn Asn Ile Leu Asn Asp Ser Lys Tyr Leu Asn Glu Asp Ser  
8480 8485 8490

Lys Tyr Gln Gln Gln Tyr Asp Arg Val Ile Ala Asp Ala Glu Gln  
8495 8500 8505

Leu Leu Asn Gln Thr Thr Asn Pro Thr Leu Glu Pro Tyr Lys Val  
8510 8515 8520

Asp Ile Val Lys Asp Asn Val Leu Ala Asn Glu Lys Ile Leu Phe  
8525 8530 8535

Gly Ala Glu Lys Leu Ser Tyr Asp Lys Ser Asn Ala Asn Asp Glu  
8540 8545 8550

Ile Lys His Met Asn Tyr Leu Asn Asn Ala Gln Lys Gln Ser Ile  
8555 8560 8565

Lys Asp Met Ile Ser His Ala Ala Leu Arg Thr Glu Val Lys Gln  
8570 8575 8580

Leu Leu Gln Gln Ala Lys Ile Leu Asp Glu Ala Met Lys Ser Leu  
8585 8590 8595

Glu Asp Lys Thr Gln Val Val Ile Thr Asp Thr Thr Leu Pro Asn  
8600 8605 8610

Tyr Thr Glu Ala Ser Glu Asp Lys Lys Glu Lys Val Asp Gln Thr  
8615 8620 8625

Val Ser His Ala Gln Ala Ile Ile Asp Lys Ile Asn Gly Ser Asn  
8630 8635 8640

Val Ser Leu Asp Gln Val Arg Gln Ala Leu Glu Gln Leu Thr Gln  
8645 8650 8655

Ala Ser Glu Asn Leu Asp Gly Asp Gln Arg Val Glu Glu Ala Lys  
8660 8665 8670

Val His Ala Asn Gln Thr Ile Asp Gln Leu Thr His Leu Asn Ser  
8675 8680 8685

Leu Gln Gln Gln Thr Ala Lys Glu Ser Val Lys Asn Ala Thr Lys  
8690 8695 8700

Leu Glu Glu Ile Ala Thr Val Ser Asn Asn Ala Gln Ala Leu Asn  
8705 8710 8715

Lys Val Met Gly Lys Leu Glu Gln Phe Ile Asn His Ala Asp Ser  
8720 8725 8730

Val Glu Asn Ser Asp Asn Tyr Arg Gln Ala Asp Asp Asp Lys Ile  
8735 8740 8745

Ile Ala Tyr Asp Glu Ala Leu Glu His Gly Gln Asp Ile Gln Lys  
8750 8755 8760

Thr Asn Ala Thr Gln Asn Glu Thr Lys Gln Ala Leu Gln Gln Leu  
8765 8770 8775

Ile Tyr Ala Glu Thr Ser Leu Asn Gly Phe Glu Arg Leu Asn His  
8780 8785 8790

Ala Arg Pro Arg Ala Leu Glu Tyr Ile Lys Ser Leu Glu Lys Ile  
8795 8800 8805

Asn Asn Ala Gln Lys Ser Ala Leu Glu Asp Lys Val Thr Gln Ser  
8810 8815 8820

His Asp Leu Leu Glu Leu Glu His Ile Val Asn Glu Gly Thr Asn  
8825 8830 8835

Leu Asn Asp Ile Met Gly Glu Leu Ala Asn Ala Ile Val Asn Asn  
8840 8845 8850

Tyr Ala Pro Thr Lys Ala Ser Ile Asn Tyr Ile Asn Ala Asp Asn  
8855 8860 8865

Leu Arg Lys Asp Asn Phe Thr Gln Ala Ile Asn Asn Ala Arg Asp  
8870 8875 8880

Ala Leu Asn Lys Thr Gln Gly Gln Asn Leu Asp Phe Asn Ala Ile  
8885 8890 8895

Asp Thr Phe Lys Asp Asp Ile Phe Lys Thr Lys Asp Ala Leu Asn  
8900 8905 8910

Gly Ile Glu Arg Leu Thr Ala Ala Lys Ser Lys Ala Glu Lys Leu  
8915 8920 8925

Ile Asp Ser Leu Lys Phe Ile Asn Lys Ala Gln Phe Thr His Ala  
8930 8935 8940

Asn Asp Glu Ile Ile Asn Thr Asn Ser Ile Ala Gln Leu Ser Arg  
8945 8950 8955

Ile Val Asn Gln Ala Phe Asp Leu Asn Asp Ala Met Lys Ser Leu  
8960 8965 8970

Arg Asp Glu Leu Asn Asn Gln Ala Phe Pro Val Gln Ala Ser Ser  
8975 8980 8985

Asn Tyr Ile Asn Ser Asp Glu Asp Leu Lys Gln Gln Phe Asp His  
8990 8995 9000

Ala Leu Ser Asn Ala Arg Lys Val Leu Ala Lys Glu Asn Gly Lys  
9005 9010 9015

Asn Leu Asp Glu Lys Gln Ile Gln Gly Leu Lys Gln Val Ile Glu  
9020 9025 9030

Asp Thr Lys Asp Ala Leu Asn Gly Ile Gln Arg Leu Ser Lys Ala  
9035 9040 9045

Lys Ala Lys Ala Ile Gln Tyr Val Gln Ser Leu Ser Tyr Ile Asn  
9050 9055 9060

Asp Ala Gln Arg His Ile Ala Glu Asn Asn Ile His Asn Ser Asp  
9065 9070 9075

Asp Leu Ser Ser Leu Ala Asn Thr Leu Ser Lys Ala Ser Asp Leu  
9080 9085 9090

Asp Asn Ala Met Lys Asp Leu Arg Asp Thr Ile Glu Ser Asn Ser  
9095 9100 9105

Thr Ser Val Pro Asn Ser Val Asn Tyr Ile Asn Ala Asp Lys Asn  
9110 9115 9120

Leu Gln Ile Glu Phe Asp Glu Ala Leu Gln Gln Ala Ser Ala Thr  
9125 9130 9135

Ser Ser Lys Thr Ser Glu Asn Pro Ala Thr Ile Glu Glu Val Leu  
9140 9145 9150

Gly Leu Ser Gln Ala Ile Tyr Asp Thr Lys Asn Ala Leu Asn Gly  
9155 9160 9165

Glu Gln Arg Leu Ala Thr Glu Lys Ser Lys Asp Leu Lys Leu Ile  
9170 9175 9180

Lys Gly Leu Lys Asp Leu Asn Lys Ala Gln Leu Glu Asp Val Thr  
9185 9190 9195

Asn Lys Val Asn Ser Ala Asn Thr Leu Thr Glu Leu Ser Gln Leu  
9200 9205 9210

Thr Gln Ser Thr Leu Glu Leu Asn Asp Lys Met Lys Leu Leu Arg  
9215 9220 9225

Asp Lys Leu Lys Thr Leu Val Asn Pro Val Lys Ala Ser Leu Asn  
9230 9235 9240

Tyr Arg Asn Ala Asp Tyr Asn Leu Lys Arg Gln Phe Asn Lys Ala  
9245 9250 9255

Leu Lys Glu Ala Lys Gly Val Leu Asn Lys Asn Ser Gly Thr Asn

9260 9265 9270

Val Asn Ile Asn Asp Ile Gln His Leu Leu Thr Gln Ile Asp Asn  
9275 9280 9285

Ala Lys Asp Gln Leu Asn Gly Glu Arg Arg Leu Lys Glu His Gln  
9290 9295 9300

Gln Lys Ser Glu Val Phe Ile Ile Lys Glu Leu Asp Ile Leu Asn  
9305 9310 9315

Asn Ala Gln Lys Ala Ala Ile Ile Asn Gln Ile Arg Ala Ser Lys  
9320 9325 9330

Asp Ile Lys Ile Ile Asn Gln Ile Val Asp Asn Ala Ile Glu Leu  
9335 9340 9345

Asn Asp Ala Met Gln Gly Leu Lys Glu His Val Ala Gln Leu Thr  
9350 9355 9360

Ala Thr Thr Lys Asp Asn Ile Glu Tyr Leu Asn Ala Asp Glu Asp  
9365 9370 9375

His Lys Leu Gln Tyr Asp Tyr Ala Ile Asn Leu Ala Asn Asn Val  
9380 9385 9390

Leu Asp Lys Glu Asn Gly Thr Asn Lys Asp Ala Asn Ile Ile Ile  
9395 9400 9405

Gly Met Ile Gln Asn Met Asp Asp Ala Arg Ala Leu Leu Asn Gly  
9410 9415 9420

Ile Glu Arg Leu Lys Asp Ala Gln Thr Lys Ala His Asn Asp Ile  
9425 9430 9435

Lys Asp Thr Leu Lys Arg Gln Leu Asp Glu Ile Glu His Ala Asn  
9440 9445 9450

Ala Thr Ser Asn Ser Lys Ala Gln Ala Lys Gln Met Val Asn Glu  
9455 9460 9465

Glu Ala Arg Lys Ala Leu Ser Asn Ile Asn Asp Ala Thr Ser Asn  
9470 9475 9480

Asp Leu Val Asn Gln Ala Lys Asp Glu Gly Gln Ser Ala Ile Glu  
9485 9490 9495

His Ile His Ala Asp Glu Leu Pro Lys Ala Lys Leu Asp Ala Asn  
9500 9505 9510

Gln Met Ile Asp Gln Lys Val Glu Asp Ile Asn His Leu Ile Ser  
9515 9520 9525

Gln Asn Pro Asn Leu Ser Asn Glu Glu Lys Asn Lys Leu Ile Ser  
9530 9535 9540

Gln Ile Asn Lys Leu Val Asn Gly Ile Lys Asn Glu Ile Gln Gln  
9545 9550 9555

Ala Ile Asn Lys Gln Gln Ile Glu Asn Ala Thr Thr Lys Leu Asp  
9560 9565 9570

Glu Val Ile Glu Thr Thr Lys Lys Leu Ile Ile Ala Lys Ala Glu  
9575 9580 9585

Ala Lys Gln Met Ile Lys Glu Leu Ser Gln Lys Lys Arg Asp Ala  
9590 9595 9600

Ile Asn Asn Asn Thr Asp Leu Thr Pro Ser Gln Lys Ala His Ala  
9605 9610 9615

Leu Ala Asp Ile Asp Lys Thr Glu Lys Asp Ala Leu Gln His Ile  
9620 9625 9630

Glu Asn Ser Asn Ser Ile Asp Asp Ile Asn Asn Asn Lys Glu His  
9635 9640 9645

Ala Phe Asn Thr Leu Ala His Ile Ile Ile Trp Asp Thr Asp Gln  
9650 9655 9660

Gln Pro Leu Val Phe Glu Leu Pro Glu Leu Ser Leu Gln Asn Ala  
9665 9670 9675

Leu Val Thr Ser Glu Val Val Val His Arg Asp Glu Thr Ile Ser  
9680 9685 9690

Leu Glu Ser Ile Ile Gly Ala Met Thr Leu Thr Asp Glu Leu Lys  
9695 9700 9705

Val Asn Ile Val Ser Leu Pro Asn Thr Asp Lys Val Ala Asp His  
9710 9715 9720

Leu Thr Ala Lys Val Lys Val Ile Leu Ala Asp Gly Ser Tyr Val  
9725 9730 9735

Thr Val Asn Val Pro Val Lys Val Val Glu Lys Glu Leu Gln Ile  
9740 9745 9750

Ala Lys Lys Asp Ala Ile Lys Thr Ile Asp Val Leu Val Lys Gln  
9755 9760 9765

Lys Ile Lys Asp Ile Asp Ser Asn Asn Glu Leu Thr Ser Thr Gln  
9770 9775 9780

Arg Glu Asp Ala Lys Ala Glu Ile Glu Arg Leu Lys Lys Gln Ala  
9785 9790 9795

Ile Asp Lys Val Asn His Ser Lys Ser Ile Lys Asp Ile Glu Thr  
9800 9805 9810

Val Lys Arg Thr Asp Phe Glu Glu Ile Asp Gln Phe Asp Pro Lys  
9815 9820 9825

Arg Phe Thr Leu Asn Lys Ala Lys Lys Asp Ile Ile Thr Asp Val  
9830 9835 9840

Asn Thr Gln Ile Gln Asn Gly Phe Lys Glu Ile Glu Thr Ile Lys  
9845 9850 9855

Gly Leu Thr Ser Asn Glu Lys Thr Gln Phe Asp Lys Gln Leu Thr  
9860 9865 9870

Ala Leu Gln Lys Glu Phe Leu Glu Lys Val Glu His Ala His Asn  
9875 9880 9885

Leu Val Glu Leu Asn Gln Leu Gln Gln Glu Phe Asn Asn Arg Tyr  
9890 9895 9900

Lys His Ile Leu Asn Gln Ala His Leu Leu Gly Glu Lys His Ile  
9905 9910 9915

Ala Glu His Lys Leu Gly Tyr Val Val Val Asn Lys Thr Gln Gln  
9920 9925 9930

Ile Leu Asn Asn Gln Ser Ala Ser Tyr Phe Ile Lys Gln Trp Ala  
9935 9940 9945

Leu Asp Arg Ile Lys Gln Ile Gln Leu Glu Thr Met Asn Ser Ile  
9950 9955 9960

Arg Gly Ala His Thr Val Gln Asp Val His Lys Ala Leu Leu Gln  
9965 9970 9975

Gly Ile Glu Gln Ile Leu Lys Val Asn Val Ser Ile Ile Asn Gln  
9980 9985 9990

Ser Phe Asn Asp Ser Leu His Asn Phe Asn Tyr Leu His Ser Lys  
9995 10000 10005

Phe Asp Ala Arg Leu Arg Glu Lys Asp Val Ala Asn His Ile Val  
10010 10015 10020

Gln Thr Glu Thr Phe Lys Glu Val Leu Lys Gly Thr Gly Val Glu  
10025 10030 10035

Pro Gly Lys Ile Asn Lys Glu Thr Gln Gln Pro Lys Leu His Lys  
10040 10045 10050

Asn Asp Asn Asp Ser Leu Phe Lys His Leu Val Asp Asn Phe Gly  
10055 10060 10065

Lys Thr Val Gly Val Ile Thr Leu Thr Gly Leu Leu Ser Ser Phe  
10070 10075 10080

Trp Leu Val Leu Ala Lys Arg Arg Lys Lys Glu Glu Glu Glu Lys  
10085 10090 10095

Gln Ser Ile Lys Asn His His Lys Asp Ile Arg Leu Ser Asp Thr  
10100 10105 10110

Asp Lys Ile Asp Pro Ile Val Ile Thr Lys Arg Lys Ile Asp Lys

10115

10120

10125

Glu Glu Gln Ile Gln Asn Asp Asp Lys His Ser Ile Pro Val Ala  
10130 10135 10140

Lys His Lys Lys Ser Lys Glu Lys Gln Leu Ser Glu Glu Asp Ile  
10145 10150 10155

His Ser Ile Pro Val Val Lys Arg Lys Gln Asn Ser Asp Asn Lys  
10160 10165 10170

Asp Thr Lys Gln Lys Lys Val Thr Ser Lys Lys Lys Thr Pro  
10175 10180 10185

Gln Ser Thr Lys Lys Val Val Lys Thr Lys Lys Arg Ser Lys Lys  
10190 10195 10200

<210> 24

<211> 1973

<212> PRT

<213> *Staphylococcus epidermidis*

<400> 24

Met Lys Glu Asn Lys Arg Lys Asn Asn Leu Asp Lys Asn Asn Thr Arg  
1 5 10 15

Phe Ser Ile Arg Lys Tyr Gln Gly Tyr Gly Ala Thr Ser Val Ala Ile  
20 25 30

Ile Gly Phe Ile Ile Ser Cys Phe Ser Glu Ala Lys Ala Asp Ser  
35 40 45

Asp Lys His Glu Ile Lys Ser His Gln Gln Ser Met Thr Asn His Leu  
50 55 60

Thr Thr Leu Pro Ser Asp Asn Gln Glu Asn Thr Ser Asn Asn Glu Phe  
65 70 75 80

Asn Asn Arg Asn His Asp Ile Ser His Leu Ser Leu Asn Lys Ser Ile  
85 90 95

Gln Met Asp Glu Leu Lys Lys Leu Ile Lys Gln Tyr Lys Ala Ile Asn  
100 105 110

Leu Asn Asp Lys Thr Glu Glu Ser Ile Lys Leu Phe Gln Ser Asp Leu  
115 120 125

Val Gln Ala Glu Ser Leu Ile Asn Asn Pro Gln Ser Gln Gln His Val  
130 135 140

Asp Ala Phe Tyr His Lys Phe Leu Asn Ser Ala Gly Lys Leu Arg Lys  
145 150 155 160

Lys Glu Thr Val Ser Ile Lys His Glu Arg Ser Glu Ser Asn Thr Tyr  
165 170 175

Arg Leu Gly Asp Glu Val Arg Ser Gln Thr Phe Ser His Ile Arg His  
180 185 190

Lys Arg Asn Ala Val Ser Phe Arg Asn Ala Asp Gln Ser Asn Leu Ser  
195 200 205

Thr Asp Pro Leu Lys Ala Asn Glu Ile Asn Pro Glu Ile Gln Asn Gly  
210 215 220

Asn Phe Ser Gln Val Ser Gly Gly Pro Leu Pro Thr Ser Ser Lys Arg  
225 230 235 240

Leu Thr Val Val Thr Asn Val Asp Asn Trp His Ser Tyr Ser Thr Asp  
245 250 255

Pro Asn Pro Glu Tyr Pro Met Phe Tyr Thr Thr Thr Ala Val Asn Tyr  
260 265 270

Pro Asn Phe Met Ser Asn Gly Asn Ala Pro Tyr Gly Val Ile Leu Gly  
275 280 285

Arg Thr Thr Asp Gly Trp Asn Arg Asn Val Ile Asp Ser Lys Val Ala  
290 295 300

Gly Ile Tyr Gln Asp Ile Asp Val Val Pro Gly Ser Glu Leu Asn Val  
305 310 315 320

Asn Phe Ile Ser Thr Ser Pro Val Phe Ser Asp Gly Ala Ala Gly Ala  
325 330 335

Lys Leu Lys Ile Ser Asn Val Glu Gln Asn Arg Val Leu Phe Asp Ser  
340 345 350

Arg Leu Asn Gly Met Gly Pro Tyr Pro Thr Gly Lys Leu Ser Ala Met  
355 360 365

Val Asn Ile Pro Asn Asp Ile Asn Arg Val Arg Ile Ser Phe Leu Pro  
370 375 380

Val Ser Ser Thr Gly Arg Val Ser Val Gln Arg Ser Ser Arg Glu His  
385 390 395 400

Gly Phe Gly Asp Asn Ser Ser Tyr Tyr His Gly Gly Ser Val Ser Asp  
405 410 415

Val Arg Ile Asn Ser Gly Ser Tyr Val Val Ser Lys Val Thr Gln Arg  
420 425 430

Glu Tyr Thr Thr Arg Pro Asn Ser Ser Asn Asp Thr Phe Ala Arg Ala  
435 440 445

Thr Ile Asn Leu Ser Val Glu Asn Lys Gly His Asn Gln Ser Lys Asp  
450 455 460

Thr Tyr Tyr Glu Val Ile Leu Pro Gln Asn Ser Arg Leu Ile Ser Thr  
465 470 475 480

Arg Gly Gly Ser Gly Asn Tyr Asn Asn Ala Thr Asn Lys Leu Ser Ile  
485 490 495

Arg Leu Asp Asn Leu Asn Pro Gly Asp Arg Arg Asp Ile Ser Tyr Thr  
500 505 510

Val Asp Phe Glu Ser Ser Ser Pro Lys Leu Ile Asn Leu Asn Ala His  
515 520 525

Leu Leu Tyr Lys Thr Asn Ala Thr Phe Arg Gly Asn Asp Gly Gln Arg  
530 535 540

Thr Gly Asp Asn Ile Val Asp Leu Gln Ser Ile Ala Leu Leu Met Asn  
545 550 555 560

Lys Asp Val Leu Glu Thr Glu Leu Asn Glu Ile Asp Lys Phe Ile Arg

565

570

575

Asp Leu Asn Glu Ala Asp Phe Thr Ile Asp Ser Trp Ser Ala Leu Gln  
580 585 590

Glu Lys Met Thr Glu Gly Gly Asn Ile Leu Asn Glu Gln Gln Asn Gln  
595 600 605

Val Ala Leu Glu Asn Gln Ala Ser Gln Glu Thr Ile Asn Asn Val Thr  
610 615 620

Gln Ser Leu Glu Ile Leu Lys Asn Asn Leu Lys Tyr Lys Thr Pro Ser  
625 630 635 640

Gln Pro Ile Ile Lys Ser Asn Asn Gln Ile Pro Asn Ile Thr Ile Ser  
645 650 655

Pro Ala Asp Lys Ala Asp Lys Leu Thr Ile Thr Tyr Gln Asn Thr Asp  
660 665 670

Asn Glu Ser Ala Ser Ile Ile Gly Asn Lys Leu Asn Asn Gln Trp Ser  
675 680 685

Leu Asn Asn Asn Ile Pro Gly Ile Glu Ile Asp Met Gln Thr Gly Leu  
690 695 700

Val Thr Ile Asp Tyr Lys Ala Val Tyr Pro Glu Ser Val Val Gly Ala  
705 710 715 720

Asn Asp Lys Thr Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr  
725 730 735

Met Pro Arg Lys Glu Ala Thr Pro Leu Ser Pro Ile Val Glu Ala Asn  
740 745 750

Glu Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln  
755 760 765

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu Val  
770 775 780

Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile Asp Tyr  
785 790 795 800

Val Asn Ile Glu Glu Asn Ser Gly Lys Val Thr Ile Gly Tyr Gln Ala  
805 810 815

Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr Lys Gly Asn Ser  
820 825 830

Asp Glu Ser Ala Glu Ser Arg Val Thr Met Pro Arg Lys Glu Ala Thr  
835 840 845

Pro His Ser Pro Ile Val Glu Ala Asn Glu Glu His Val Asn Val Thr  
850 855 860

Ile Ala Pro Asn Gly Glu Ala Thr Gln Ile Ala Ile Lys Tyr Arg Thr  
865 870 875 880

Pro Asp Gly Gln Glu Thr Thr Leu Ile Ala Ser Lys Asn Gly Ser Ser  
885 890 895

Trp Thr Leu Asn Lys Gln Ile Asp Tyr Val Asn Ile Glu Glu Asn Ser  
900 905 910

Gly Lys Val Thr Ile Gly Tyr Gln Ala Val Gln Leu Glu Ser Glu Val  
915 920 925

Ile Ala Thr Glu Thr Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg  
930 935 940

Ile Thr Met Leu Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu  
945 950 955 960

Ala Asn Glu Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Ala  
965 970 975

Thr Gln Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr  
980 985 990

Leu Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile  
995 1000 1005

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1010 1015 1020

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr  
1025 1030 1035

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro  
1040 1045 1050

Arg Lys Glu Ala Thr Pro Ile Pro Pro Thr Leu Glu Ala Ser Val  
1055 1060 1065

Gln Glu Ala Ser Val Thr Val Thr Pro Asn Glu Asn Ala Thr Lys  
1070 1075 1080

Val Phe Ile Lys Tyr Leu Asp Ile Asn Asp Glu Ile Ser Thr Ile  
1085 1090 1095

Ile Ala Ser Lys Ile Asn Gln Gln Trp Thr Leu Asn Lys Asp Asn  
1100 1105 1110

Phe Gly Ile Lys Ile Asn Pro Leu Thr Gly Lys Val Ile Ile Ser  
1115 1120 1125

Tyr Val Ala Val Gln Pro Glu Ser Asp Val Ile Ala Ile Glu Ser  
1130 1135 1140

Gln Gly Asn Ser Asp Leu Ser Glu Glu Ser Arg Ile Ile Met Pro  
1145 1150 1155

Thr Lys Glu Glu Pro Pro Glu Pro Pro Ile Leu Glu Ser Asp Ser  
1160 1165 1170

Ile Glu Ala Lys Val Asn Ile Phe Pro Asn Asp Glu Ala Thr Arg  
1175 1180 1185

Ile Val Ile Met Tyr Thr Ser Leu Glu Gly Gln Glu Ala Thr Leu  
1190 1195 1200

Val Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile  
1205 1210 1215

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1220 1225 1230

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr  
1235 1240 1245

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Val Thr Met Pro  
1250 1255 1260

Arg Lys Glu Ala Thr Pro His Ser Pro Ile Val Glu Thr Asn Glu  
1265 1270 1275

Glu Arg Val Asn Val Val Ile Ala Pro Asn Gly Glu Ala Thr Gln  
1280 1285 1290

Ile Ala Ile Lys Tyr Arg Thr Pro Asp Gly Gln Glu Thr Thr Leu  
1295 1300 1305

Ile Ala Ser Lys Asn Gly Ser Ser Trp Thr Leu Asn Lys Gln Ile  
1310 1315 1320

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1325 1330 1335

Tyr Gln Ala Val Gln Pro Glu Ser Glu Ile Ile Ala Thr Glu Thr  
1340 1345 1350

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro  
1355 1360 1365

Arg Lys Glu Ala Ile Pro His Ser Pro Ile Val Glu Ala Asn Glu  
1370 1375 1380

Glu His Val Asn Val Thr Ile Ala Pro Asn Gly Glu Thr Thr Gln  
1385 1390 1395

Ile Ala Val Lys Tyr Arg Thr Pro Asp Gly Gln Glu Ala Thr Leu  
1400 1405 1410

Ile Ala Ser Lys Asn Glu Ser Ser Trp Thr Leu Asn Lys Gln Ile  
1415 1420 1425

Asp His Val Asn Ile Asp Glu Asn Ser Gly Lys Val Thr Ile Gly  
1430 1435 1440

Tyr Gln Ala Val Gln Pro Glu Ser Glu Val Ile Ala Thr Glu Thr

1445 1450 1455

Lys Gly Asn Ser Asp Ala Ser Ala Glu Ser Arg Ile Thr Met Pro  
1460 1465 1470

Val Lys Glu Lys Thr Pro Ala Pro Pro Ile Ser Ile Ile Asn Glu  
1475 1480 1485

Ser Asn Ala Ser Val Glu Ile Ile Pro Gln Val Asn Val Thr Gln  
1490 1495 1500

Leu Ser Leu Gln Tyr Ile Asp Ala Lys Gly Gln Gln Gln Asn Leu  
1505 1510 1515

Ile Ala Thr Leu Asn Gln Asn Gln Trp Thr Leu Asn Lys Asn Val  
1520 1525 1530

Ser His Ile Thr Val Asp Lys Asn Thr Gly Lys Val Leu Ile Asn  
1535 1540 1545

Tyr Gln Ala Val Tyr Pro Glu Ser Glu Val Ile Ala Arg Glu Ser  
1550 1555 1560

Lys Gly Asn Ser Asp Ser Ser Asn Val Ser Met Val Ile Met Pro  
1565 1570 1575

Arg Lys Thr Ala Thr Pro Lys Pro Pro Ile Ile Lys Val Asp Glu  
1580 1585 1590

Met Asn Ala Ser Leu Ala Ile Ile Pro Tyr Lys Asn Asn Thr Ala  
1595 1600 1605

Ile Asn Ile His Tyr Ile Asp Lys Lys Gly Ile Lys Ser Met Val  
1610 1615 1620

Thr Ala Ile Lys Asn Asn Asp Gln Trp Gln Leu Asp Glu Lys Ile  
1625 1630 1635

Lys Tyr Val Lys Ile Asp Ala Lys Thr Gly Thr Val Ile Ile Asn  
1640 1645 1650

Tyr Gln Ile Val Gln Glu Asn Ser Glu Ile Ile Ala Thr Ala Ile  
1655 1660 1665

Asn Gly Asn Ser Asp Lys Ser Glu Glu Val Lys Val Leu Met Pro  
1670 1675 1680

Ile Lys Glu Phe Thr Pro Leu Ala Pro Leu Leu Glu Thr Asn Tyr  
1685 1690 1695

Lys Lys Ala Thr Val Ser Ile Leu Pro Gln Ser Asn Ala Thr Lys  
1700 1705 1710

Leu Asp Phe Lys Tyr Arg Asp Lys Lys Gly Asp Ser Lys Ile Ile  
1715 1720 1725

Ile Val Lys Arg Phe Lys Asn Ile Trp Lys Ala Asn Glu Gln Ile  
1730 1735 1740

Ser Gly Val Thr Ile Asn Pro Glu Phe Gly Gln Val Val Ile Asn  
1745 1750 1755

Tyr Gln Ala Val Tyr Pro Glu Ser Asp Ile Leu Ala Ala Gln Tyr  
1760 1765 1770

Val Gly Asn Ser Asp Ala Ser Glu Trp Ala Lys Val Lys Met Pro  
1775 1780 1785

Lys Lys Glu Leu Ala Pro His Ser Pro Ser Leu Ile Tyr Asp Asn  
1790 1795 1800

Arg Asn Asn Lys Ile Leu Ile Ala Pro Asn Ser Asn Ala Thr Glu  
1805 1810 1815

Met Glu Leu Ser Tyr Val Asp Lys Asn Asn Gln Ser Leu Lys Val  
1820 1825 1830

Lys Ala Leu Lys Ile Asn Asn Arg Trp Lys Phe Asp Ser Ser Val  
1835 1840 1845

Ser Asn Ile Ser Ile Asn Pro Asn Thr Gly Lys Ile Val Leu Gln  
1850 1855 1860

Pro Gln Phe Leu Leu Thr Asn Ser Lys Ile Ile Val Phe Ala Lys  
1865 1870 1875

Lys Gly Asn Ser Asp Ala Ser Ile Ser Val Ser Leu Arg Val Pro  
1880 1885 1890

Ala Val Lys Lys Ile Glu Leu Glu Pro Met Phe Asn Val Pro Val  
1895 1900 1905

Leu Val Ser Leu Asn Lys Lys Arg Ile Gln Phe Asp Asp Cys Ser  
1910 1915 1920

Gly Val Lys Asn Cys Leu Asn Lys Gln Ile Ser Lys Thr Gln Leu  
1925 1930 1935

Pro Asp Thr Gly Tyr Ser Asp Lys Ala Ser Lys Ser Asn Ile Leu  
1940 1945 1950

Ser Val Leu Leu Leu Gly Phe Gly Phe Leu Ser Tyr Ser Arg Lys  
1955 1960 1965

Arg Lys Glu Lys Gln  
1970